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11028.050 Million cell updates/sec
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     GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX702273	RESULT 1
Muralidhara, P. Novel gpcr-like proteins and nucleic acids encoding same	Casman, S.J., Edinger, S.R., Ellerman, K., Smithson, G., Kekuda, R. and		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	•	AX702273.1 GI:29537547	AX702273	Sequence 33 from Patent WO02064793.	AX702273 1104 bp DNA linear PAT 03-APR-2003		

ALIGNMENTS

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                AAGCTGTGCAGCACAGCTCGGGAGGACCAGTGACCAGGAGAAAGGACGCCACTGGCGA
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/mol_type="unassigned DNJ
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                                                                  GCATCCACCCATTACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCC
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                                                                              /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="13"
/clone="RP11-178C10"
 /note="L1MB8 repeat: matches 5836. .6160 656. .723 /note="L2 repeat: matches 2592. .2659 of
                                                                                                                                                                              Location/Qualifiers
                                                /clone_lib="RPCI-11.1"
l61. .463
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On Apr 12, 2001 this sequence version replaced gi:13276997.
On Apr 12, 2001 this sequence version replaced from overlapping clones.
Where differences are found these are annotated as variations
where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em. EMBL; Sw:,
SWISSPROT; Tr. TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr13

RP11-178C10 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBaCe3.6
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IMPORTANT: This sequence is not the entire insert of clone RP11-178C10 It may be shorter because we sequence overlappir sections only once, except for a 100 base overlap. The true right end of clone RP11-178C10 is at 98861 in this sequence. The true right end of clone RP11-461N23 is at 100 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Libration" repeat: matches 5264. .5577 of consensus" 12181. .12626
/note="Libration" repeat: matches 3474. .3949 of consensus" 12649. .13012.
/note="Libration" repeat: matches 5571. .5927 of consensus" 13491. .14076
/note="Libration" repeat: matches 2226. .2881 of consensus" 16310. .17185
/note="Libration" repeat: matches 6237. .7151 of consensus" 17207. .1762e "Libration" repeat: matches 7197. .7157 of consensus" 17628. .18380
/note="Libration" repeat: matches 7197. .7976 of consensus" 17628. .18380
/note="Libration" repeat: matches 7197. .7976 of consensus" 20797. .21100
                                                                                                                                                                             215. .6548
note="Charliel repeat: matches 2292. .2629 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="W12 repeat: matches 196. .251 of consensus"
5982. .26012
note="Tigger4(Zombi) repeat: matches 2701. .2731 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6005. .26208
note="Tigger4(Zombi) repeat: matches 1772. .1970 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Alux repeat: matches 1. .297 of consensus"
2746. .22814
note="Lz repeat: matches 2574. .2643 of consensus"
3758. .23981
                                                                                                                               859. 5987
note="L2 repeat: matches 2574. .2708 of consensus"
                                                                                                                                                                                                                    557, .6635
note="L2 repeat: matches 2128. .2206 of consensus"
                                                                                                                                                                                                                                                                                     note="L2 repeat: matches 1330. .1889 of consensus"
                                                                                                                                                                                                                                                                                                                                                   893. .8994
note="L2 repeat: matches 1551. .1656 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                             554. .9754
note="MER20 repeat: matches 33. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluJb repeat: matches 85. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2570, .2688 of consensus"
5740, .25795
                                                                 note="L2 repeat: matches 1031. .1120 of consensus"
385. .2420
note="MIR repeat: matches 111. .146 of consensus"
                                                                                 989, .5306.
note="WER7A repeat: matches 2. .345 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6209. .26513
note="AluSx repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Alusq repeat: matches 1. .313 of consensus" 9481. .39767
note="Alusx repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                          301. 8499 note="MIR repeat: matches 17. .219 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56514. .28201
/note="Tigger4(Zombi) repeat: matches 1. .1772 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="THEIC repeat: matches 1. .58 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          816. .9979
mote="FAM repeat: matches 2. .165 of consensus"
0402. .10703
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fnote="15 copies 2 mer ac 100% conserved"
6220. .35303
fnote="2 copies 42 mer 97% conserved"
16967. .37274
                                                                                                                                                                                                                                                                                                                                                                                               079. .9126 _
note="24 copies 2 mer at 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41084, .41111
/note="14 copies 2 mer aa 89% conserved"
41119, .41174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1616. .32843
Note="6 copies 38 mer 86% conserved"
                                        .4646
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hote="LIME3A repeat: matches 5789. .6157 of consensus"
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/note="LiME3A repeat: matches 5301. .5782 of consensus"
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/note="L1PA6 repeat: matches 2744. .6141 of consensus"
11364. .51523
/note="MERSA repeat: matches 1. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluSg/x repeat: matches 163. .300 of consensus"
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Best Local Similarity 83.6%; Pred. No. 7.6e-149;
Matches 1006; Conservative 0; Mismatches 0; Indels 197; Gaps
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fnote="MLTIG repeat: matches 169. .264 of consensus"
37561. .58049
/note="MER74A repeat: matches 1. .519 of consensus"
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note="MLTIF repeat: matches 437. .541 of consensus"
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5/00te="MER74A repeat: matches 1. .139 of consensus"

5/337. .59435

fnote="MLTIG repeat: matches 169. .264 of consensus"
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/note="MLTIF repeat: matches 437. .541 of consensus"
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note="WER21B repeat: matches 41. .789 of consensus"
4321. .54629
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                                                      /note="THEIC repeat: matches 58. .344 of consensus" 41791. .41842

Ante="L2 repeat: matches 1215. .1266 of consensus" 42051. .42573 /note="MER74A repeat: matches 2. .555 of consensus" /note="MER74A repeat: matches 2. .555 of consensus"
                                                                                                                                                          Anote="MITIC repeat: matches 1, .466 of consensus" 44860. .45175
/note="MIT2FB repeat: matches 1. .328 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MLTIG repeat: matches 76. .205 of consensus"
58496. .58809
                   note="AluSp repeat: matches 1. .309 of consensus" 1483. .41785
                                                                                                                                                                                                                                                                                                                   45204. .45235
/note="16 copies 2 mer tg 87% conserved"
45389. .45559
/note="MERSB repeat: matches 4. .175 of consensus"
45639 . .45788
/note="MERSA repeat: matches 9. .184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1848. .>216/
note="MSTB repeat: matches 86. .422 of consensus"
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1848. .52167
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Oy 1042 CAGGCCAGAGGTTCTA 	RESULT 4 ACO16189 LOCUG DOCUS DEFINITION Homo sapiens clone ACCESSION ACO16189.3 G1:912 VERSION ACO16189.3 G1:912 KEYWORDS HTG; HTGS_PHASEO. SOURCE Homo sapiens (huma ORGANISM HOmo sapiens (huma	Mammajia, Butheria REFERENCE 1 (Dases 1 to 151 AUTHORS Birren, B., initron, TITLE Unpublished REFERENCE 2 (Dases 1 to 151 AUTHORS Birren, B., initron, Birren, B., initron, Brown, A., Castle, Brown, A., Castle, Cooke, P., DeArella	Ferreira,P., Filtz Galagan,J., Gardyr Howland,J.C., John Lehoczky,J., Lieu, McEwan,P., McGurk, Morrow,J., Naylor, Peterson,K., Pollar Stange-Thomann,N.,	Tesfayo., Tirrel Wyman,D., Ye,W.J., TITLE Direct Submission JOURNAL Submitted (23-NOV- Research, 320 Chan		Web site: http://www.contacts.segurer.com/conter project/Conter project/Conter project/Conter clone 1	* sequencing read * contigs. Runs o * and the order il * arbitrary. Low- * identifying clo * voerlap relatio * However, it sho * However, it sho * the record is u	* be preserved. * 1 852 * 952 18 * 1805 19 * 1905 27 * 2720 28
56922 CGCTCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTT 56863	277 GGCTCCAGCTGGCCAAGGGGCTCTGCAAGGCTAACGGCGTTTGTGCTCTACACC 336	56623 GTCTGTGTCCACTGGGGCCCCCGGCCACGGCCAGGCCAG		679	56263 GGCCACCGGGGGCAGCCCAGGAGCCCAGGGGGAAAGGAAACGCACCGGCA 56204 679 670	682 56143 742	SECURATE SECURATE SECURATION OF THE SECURATION OF SECURA	922 GCATCCACCATTACAGGAAATGGCTCCTGGGCATTTTAAAGCTCCAAAGGGTCTTCCTCC 981
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nton, i., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Strle, A., Colangelo, M., Collins, S., Collymore, A., Krellano, K., Domino, M., Domelan, L., Doyle, M., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Bardyna, S., Grant, G., Raon, E., Karatas, A., Horton, L., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Wiley, R., McKernan, C. H., O'Connor, T., O'Donnell, P., Pollara, V., Riley, R., Suy, A., Santos, R., Severy, P., H., Subramanian, A., Talamas, J., Hirell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Hir, J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., ATGITCITAGCGGAGCACGTGGTCTAACGTGTCATTTGCTTTATG 1101 151174 bp DNA linear HTG 13-JUL-2000 ne RP11-23M9, LOW-PASS SEQUENCE SAMPLING. 70.-1999) Whitehead Institute/MIT Center for Genome harles Street, Cambridge, MA 02141, USA this sequence version replaced gi:6939915.

i dentified using RepeatMasker:

3reen, P. (1996-1997)

me.washington.edu/RM/RepeatMasker.html

3enome Center

Genome Center

Genome Research

HBR. ba; Chordata; Craniata; Vertebrata; Euteleostomi; la; Primates; Catarrhini; Hominidae; Homo. 51174) record contains 152 individual reads that have not been assembled into ns of N are used to separate the reads er in which they appear is completely clow-pass sequence sampling is useful for clones that may be gene-rich and allows ationships among clones to be deduced. Should not be assumed that this clone uenced to completion. In the event that is updated, the accession number will itp://www-seq.wi.mit.edu
puence submissions@genome.wi.mit.edu
project Information
ict name: L4399 f 100 bp g of 853 bp in length f 100 bp f 100 bp in length g of 815 bp in length f 100 bp n,L., Nusbaum,C. and Lander,E. 851: contig o 951: gap of 1 1804: contig o 1904: gap of 1 2719: contig o 2819: gap of 1 29134 31174) nan)

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126 CTTCAGTGCCCTGGGAAACATCCTTGCCTTTGCCTTACCTGTCA-AAAGAGCAGGAAGA 184

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126 464 306 643 703 425

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PAT 28-SEP-2001
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0166750.A 64 13-SEP-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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Sequence 64 from Patent WO0166750.
AX244735 GI:15859614
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/organism="Homo sapiens"
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Best Local Similarity 98.8
Matches 403; Conservative
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Mammalia, Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                               138935 GCACGGCTGGCCGCCCAGGCTGGTCTGCGTGGCCATCTGGACCTTGGTGCTGCTGCAGA
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Novel g protein-coupled receptors
Patent: WO 0162797-A 35 30-AUG-2001;
PHARWACIA & UPJOHN COMPANY (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 397.2; DB 6;
Pred. No. 7.7e-71;
0; Mismatches 8;
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    .536
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 35 from Patent WO0162797.
AX230148
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Saldwin, J., Barna, N., Beckerly, R., Boqualavky, L., Boukhgalter, B.,
Baldwin, J., Barna, N., Beckerly, R., Boqualavky, L., Boukhgalter, B.,
Baddwin, J., Barna, N., Beckerly, R., Boqualavky, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L.,
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Galagan, J., Gardyna, S., Grant, G., Funke, R., Gage, D.,
Intended, J.C., Johnson, R., Jones, C., Kana, L., Karatas, A., Klein, J.,
McMan, D., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
McTow, J., Naylor, J., Locke, K., Macdonald, P., Marquis, N.,
McTow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vasslikev, H., Vo, A., Wheeler, J., Wu, X.,
Direct Submission

All Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6939915.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                           997 ICCICCACCCCAGGAAAAGCTICTICAGAAACACCCAAGTATCACCCAGGCCAGAGGTTCT 1056
                                                                                                                                                                                                                                                                                                                                                 linear HTG 13-JUL-2000
                             317 AGGABATGGCTCCTGGGCATTTTAAAGCTCAAAGGGCTCT---TCCTCCTCCTCCTCCTCC 261
                                                                                                                   260 TCCTCCACCCCAGGABAAGCTTCTTCAGAAACACCAAGTATCACCCAGGCCAGAGGTTCT 201
  Eukaryofe, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 151174)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-23M9

Unpublished
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Center: Whitehead Institute/ MIT Center for Genome Research
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Homo sapiens clone RP11-23M9, LOW-PASS SEQUENCE SAMPLING,
ACULE189
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
                                                                                                                                                                                   1057 ATGITCTTAGCGGAGCACGTGGTCTAACGTGTCATTGCTTTATGACT 1104
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L4399
Center clone name: 23_M_9
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HTG; HTGS_PHASE0.
Homo sapiens (human)
Homo sapiens
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BX470183 162543 bp DNA linear HTG 04-AUG-2003
Danio rerio clone CH211-184M13, WORKING DRAFT SEQUENCE, 4 unordered
                                                                                                               ATGGCGAGAGGGATGCTCCACCTGCCATCCTGTGCCGAGCGGAGGGCTTTCTTACTGTCC 858
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Submitted (03-AUG-2003) Wellcome Trust Sanger Institute, Hinxton,
Submitted (03-AUG-2003) Wellcome Trust Sanger Institute, Hinxton,
zfish-help@sanger.co.uk
On Aug 4, 2003 this sequence version replaced gi:30424174.
Center: Wellcome Trust Sanger Institute
Center code: SC
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Estinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae; Danio.
1 (bases 1 to 162543)
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107248 CTTCAGGCCACCGTGGCCCTCATGAACATGAACTGTGGCATTACCCC-ATCATTTACTTC
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                            107428 GIAGGAITCAGITCCCAGCAGIAAAGCACCGCCICIGCCGAGGCIGCCIGTCTACGCIGC
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                                                           TGATGCTGGTGGCCGTGGTCTGCTTCAGCCCCTACCA-CCTCAACATCAAGCAGTTC
        ggaggcccagtgaccagcaggaaaggac-gccactggcgaggctgcctgcttacgctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Chemistry: Dye-terminator; 100% of reads Consensus quality: 162049 bases at least Q40 Consensus quality: 162049 bases at least Q30 Consensus quality: 162049 bases at least Q20 Insert size: 162243; sum-of-contigs at least part size: 177307; 8.8% error; agarcse-fp Quality coverage: 8.74x in Q20 bases; sum-of-contigs Quality coverage: 8.00x in Q20 bases; agarcse-fp
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BX470183.3 GI:33438489
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
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gap of 100 bp
contig of 846 bp in length
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contig of 813 bp in length
gap of 100 bp in length
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       gap of 100 bp contig of 842 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp contig of 837 bp in length gap of 100 bp contig of 851 bp in length gap of 100 bp in length
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g of 852 bp in length
f 100 bp
g of 849 bp in length
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of 879 bp in length
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826 bp in length
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Pred. No. 8.2e-62;
0; Mismatches 16;
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Best Local Similarity 95.3%;
Matches 407; Conservative
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389063:
390645:
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* NOTE: This is a 'working draft' sequence. It currently

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Indels

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dakrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Garnd-Pierre, N., Gande, S., Gorde, S., Govete, M., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacCarthy, M., McGwan, P., McKernan, K., Marquis, N., Mathews, C., MacCarthy, M., McGwan, P., McKernan, K., McPheeters, R., Meldrim, J., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Nayor, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymon, C., Roeetti, M., Roy, A., Santos, R., Schuer, S., Schuer, S., Schuer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stanan, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, V., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Jinect Submission

All Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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     133070 GACCTGGTCATCGAACGTGCATGGAGTTCTCCAATTTTGACAG---CAAGAGGATGGCCT 133014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC102718 190588 bp DNA linear HTG 14-JUN-2003
Mus musculus clone RP24-469E6, WORKING DRAFT SEQUENCE, 9 unordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 190588)
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                                                                                                    133013 ATGİTCİNÇIÇILICGÇILGÇĞILİRİĞĞĞİTTİTCATĞCÇATĞĞĞACİTAİTÇİTİĞÇİ
                                                                                                                                                        GCTATATGAAGATCACCTGGAAGCTGTGCAGCACAGCTCGGGAGGACCCAGTGACCAGCA
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AC102718.3 GI:31745314
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 261.2; DB 2; Length 162543;
Pred. No. 5.8e-43;
                                                                                                                                                                                            1 5005: contig of 5005 bp in length
506 5105: gap of 100 bp
541 101640: contig of 96435 bp in length
641 156970: contig of 55330 bp in length
971 157070: gap of 100 bp
157070: gap of 100 bp
1771 162543: contig of 5473 bp in length.
Location/Qualifiers
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/clone=lib="CHORI-211"
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fragment_chali:1
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/note="assembly fragment:01214
fragment_chain:2"
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Signates 1 to 190588)

Sirren, B., Nuchabun, C., Lander, E., Abouelleil, A., Allen, N., Bairen, B., Nuchabun, C., Lander, B., Camarata, J., Chang, J., Choopel, Y., Bogalavkiy, L., Boukhgalter, B., Carma, B., Dekrellano, K., Collymore, A., Cock, A., Cocke, P., Corum, B., Dekrellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dortis, L., Erickson, J., Faro, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand, Flexe, N., Hafez, N., Hagoshan, J., Hayosh B., Hall, J., Horton, L., Hulme, W., Ilier, T., Johnson, R., Jones, C., Linders, T., Levine, R., Linde, J., Macdeni, C., Macchen, C., Macchen, Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Chub, M., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, W., Stobban, S., Stubbs, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyasnilev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wann, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M., Direct Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-UN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 14, 2003 this sequence version replaced g1:22381711.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project name: 119343
Center clone name: 469 E 6
Sequencing vector: plasmid; n/a; 100% of reads
Center clone name: 469 E 6
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 187732 bases at least Q40
Consensus quality: 189782 bases at least Q30
Consensus quality: 189429 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 189788; num.of.contigs
Quality coverage: 10.2 in Q20 bases; sum-of-contigs
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430: gap of 100 bp

970: contig of 540 bp in length

1070: gap of 100 bp

7799: contig of 6729 bp in length

7899: gap of 100 bp

6142: contig of 8243 bp in length

6242: gap of 100 bp

3388: contig of 13146 bp in length

4588: gap of 100 bp

346: contig of 13146 bp in length
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                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="kp24-469E6"
/clone lib="RPCI-24 Male Mouse BAC"
1. .330
/note="assembly_fragment
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/note="assembly_fragment"
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'note="assembly_fragment"
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                                                                                                                                                 organism="Mus musculus"
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431. .970
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Sirem, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, Brown, A., Campoplano, A., Chang, J., Changol, T., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferrelra, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyras, S., Ginde, S., Govette, M., Graham, L., Gard-Pierre, M., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lanoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McGwan, P., McKernan, K., Meldrim, J., Matthews, C., McCarthy, M., McRoga, V., Murphy, T., Naylor, S., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Naylon, C., Retta, R., Rieback, M., Riley, R., Schauber, S., Schupback, R., Seman, S., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Waman, D., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Waman, D., Ye, W.J., Young, G., Direct, Subhia, R., Vo, A., Wilson, B., Waman, D., Ye, W.J., Young, G., Direct, Subhia, R., Vo, A., Wilson, B., Wal, A., Waman, D., Ye, W.J., Young, G., Direct, Subhia, R., Vo, A., Wilson, B., Wal, A., Walland, Treatin, Leaker, Subramanian, A., Talamas, J., Ye, W.J., Young, G., Direct, Subhia, R., Vo, A., Wilson, B., Wal, M., K., Wyman, D., Ye, W.J., Young, G., Direct, Subhia, R., Vo, A., Wilson, B., Wal, W.X., Wyman, D., Ye, W.J., Young, G., Direct, Subhia, R., Vo, A., Wilson, B., Wal, Y., Wal, M., K., Wal, Leaker, M., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M., K., Wal, M.
                                                                                                                                              107860 AATCTGGTGAACAAAAAGGCTCTCAACACAATTATCCTCATTGTCGTGTTCATCC 107919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107800 GTTACTCTCAGATCTGCTGCAAACTCTTCAGGACTGCCAAGCAGAACCCACTCACGGAGA 107859
                                                                                                                                                                                                                                                                                107980 CTGGAGCCCTGGAGTGTGGGGCGAGACATTCCTTCCAGATCTCTCTGCACTTCACGGTGT 108039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC110249 25-NOV-2003
Mus musculus chromosome 14 clone RP23-25708 map 14, *** SEQUENCING
IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                         821 TGCCATCC-----TGTGCCGAGCGGAGGCTTTCTTACTGTCCCTTCAGGCCACCGTGG 874
                                                                         701 GGAAAGGACGCCACTGCCTGCTTACGCTGCTGATGCTGGTGGCCGTGGTGG 760
                                                                                                                                                                                                                           761 TCTGCTTCAGCCCCTACCACCTCAACATCAAGCAGTTCATGGCGAGAGGGATGCTCCACC 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        875 CCCTCATGAACATGAACTGTGGCATTACCCCAATCATTTACTTCTTTGCATCCACCCATT 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  935 ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCTCTT 994
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Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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Mus musculus chromosome 14, clone RP23-25708
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Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferrelara, D., Flizderand, M., Gagagan, J., Galagan, J., Grand-Perre, M., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Katagas, A., Kalls, C., Landers, T., Levine, R., Machan, C., Lindhidad-Toh, K., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Maneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Maneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Fierre, N., Ramasamy, U., Raymond, C., Retta, R., Rase, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Sasman, S., Schupback, R., Sasman, S., Schupka, M., Travers, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasillev, H., Venkataraman, V.S., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Stange-Thomann, N., Stolanovic, N., Stubbs, M., Travers, M., Vasillev, H., Venkataraman, V.S., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., Viel, R., V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 25, 2003 this sequence version replaced gi:37777380. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and the accession number will be preserved.

1 169489 169588 gap of 100 bp
168589 204438: contig of 100 bp
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/clone_lib="RPCI-23 Female Mouse BAC"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schaerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNS sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 112 Row: o Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Ereen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Lario,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-MAY-2003) National Institutes of Health, Mammalian
Submitted (27-MAY-2003) Cancer Genomics Office, National Cancer
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Dennis Taub, Dan Longo (NIA, USA),
Conathan Keller (NCI, USA)
conathan Keller (NCI, USA)
conathan Keller (NCI, USA)
Institute on Aging, NIH: http://lgamn.grc.nia.nih.gov/conA/)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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/clone="WOC:60769 IMMSE:30073287"
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/clone_lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)"
(Lin-/c-Fit-/Sca-1+)
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/db_xref="GI:31127265"
/db_xref="LocusID:321019"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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strain="C57BL/6NCr"
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TITLE
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COMMENT
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Klauener, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., March, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usddin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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                                                                                                                        CCTACGGGGGGGTCTACCTCATGGCCTGTGAGCGTGGACCATTACCCAGCTGTGGTCT
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TALVEYINIYAGVNFWTCLSIDRFFAVVHPLRYNKIKRIEXAKGVCLSVWILVFAQTL
PLFUPNSKERGDKTTCMEYPNFEGTASLPWILLGACLLGFYLLETTAKGYCLILCYSQTCK
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/translation="MANNFTTPLATSHGNNCDLYAHHSTARVLMPLHYSLVFIIGLVG
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Rattus norvegicus clone CH230-64N15, WORKING DRAFT SEQUENCE, 3
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935 ACAGGAAATGGCTCCTGGGCAFTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                             1064 TGAGGTCAGCCCTGAAGAGAGAGTCGCGGGAAATGACA 1101
                                                                                                                                            995 CCTCCTCCACCCCAGGAAAGCTTCTTCAGAAACACCA 1032
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Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                               Baylor Plaza, Houston, TX 77030, USA.
On Nov 19, 2002 this sequence version replaced gi:22771237.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence way extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                     Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                    Submitted (10-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Center project name: KANY
Center clone name: CH230-64N15
Center clone name: CH230-64N15
Assembly program: Phrap, version 0.990329
Consensus quality: 218763 bases at least Q40
Consensus quality: 220754 bases at least Q30
Consensus quality: 221894 bases at least Q20
Estimated insert size: 217944; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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7 17466: gap of unknown length
7 228779: contig of 211313 bp in length
0 228879: gap of unknown length
0 239344: contig of 10465 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center code: BCM
Web site: https://www.hgsc.bcm.tmc.edu/
Contact: hggc-help@bcm.tmc.edu
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/db_xref="taxon:10116"
/clone="CH230-64N15" '
complement(12152. .13760)
                                                                                                                                                            Rat Genome Sequencing Consortium.
Direct Submission
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13069. .14398
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Pred. No. 3.4e-32;
0; Mismatches 414;
                                                     .210084)
                                                                                                                                                                                                                                            end_sequence:BH346386"
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complement 7209286. .2.
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clone_end:T7
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Best Local Similarity 53.0%;
Matches 473; Conservative C
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12. I (Dases I to 244622).
12. MILDIN, D. MARER, M. Lee., Abramazon, S., Adams, C., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Alder, J., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., David, J., Alder, J., Alder, J., Alder, J., Marter, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Gartia, M., Aldor, J., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Jang, H., Ja
                                                                                                                                                                                                        AC094739 244625 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-5C8, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                          935 ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCC 987
                                                                                                                                                                                                                                                                                                                                     DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                     AC094739.5 GI:30466566
HTG; HTGS_PHASE2; HTGS_DRAFT;
Rattus norvegicus (Norway rat)
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                          RESULT 13
AC094739/c
LOCUS
DEFINITION
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JOURNAL
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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Say Genome Sequencing Consortium.

S. Rat Genome Sequencing Consortium.

S. Rat Genome Sequencing Consortium.

B. Direct Submission

Direct Submission

May 9, 2003 Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:22771707.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

I 244625: contig of 244625 bp in length.
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db_xref="taxon:10116"
clone="CH230-5C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
Center code: BCM
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/note="wgs_end_extension
clone_end:Sp6"
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note="clone_boundary
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complement[242705.
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Score 208.6; DB 2;
Pred. No. 3.4e-32;
0; Mismatches 414;
Query Match
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Liaw,C.W., Behan,D.P. and Chalmers,D.T.
Non-endogenous, constitutively activated human protein-coupled
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16.7%; Score 184.8; DB 6;
Best Local Similarity 50.6%; Pred. No. 2.1e-27;
Matches 475; Conservative 0; Mismatches 457;
                                                                                Patent: US 6555339-A 77 29-APR-2003;
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/organism="unknown"
/mol_type="genomic DNA"
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935 ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCT
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: EP 1286165-A 1 26-FBB-2003;
Pfizer Limited (6B); PFIZER INC. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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701 GGAAAGGACGCCACTGGCGAGGCTGCTTACGCTGCTGATGCTGGTGGCCGTGGTGG 760
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		Description	Abs64723 cDNA enco	Adc86840 Human GPC	Aak76477 Human imm	Abk94922 Human nov	Aas78869 DNA encod	Aas98131 Human DNA	Aas42840 Human G P	Aas30791 Human cDN	Aasselll Human DNA	Human	Acc48996 Human G-p	6 Human	9	Aav25491 cDNA for	Aca56681 Human sig	Ade84890 Farnesyl	Ade25635 Human cDN	Aaa30730 DNA encod	Adc22724 Human G p	Abz42660 Human EBV	Aaa52629 Eosinopih	Aas98061 Human DNA	Ach23286 Human adu
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24	25	26	27	28	29	30	31	32	33	3.4	3.5	36	3.7	38	9	40	41	4.	43	44	45

ALIGNMENTS

G protein coupled receptor related protein; ss; gene; human; GPCR; cardiomyopathy; atherosclerosis; diabetes; cancer; stroke; von Hippel-Lindau syndrome; Alzheimer; afisease; tuberous sclerosis; hypercalcaemia; parkinson's disease; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; addiction; anxiety; depression; pain; obesity; Crohn's disease; osteoporosis; haemophilia; asthma; inflammatory bowel disease; infertility; hypertension; scleroderma; arthritis; human immunodeficiency virus; autoimmune disease; HIV; 'n Kekuda Smithson G, Casman SJ, Edinger SR, Ellerman K, Muralidhara P; infection; graft-versus-host disease. CDNA encoding human GPCR16 protein. ABS64723 standard; cDNA; 1104 BP. 03-JAN-2001; 2001US-0259552P. 09-JAN-2001; 2001US-0260544P. 20-MAR-2001; 2001US-0277405P. 03-JAN-2002; 2002WO-US000056. (first entry) (CURA-) CURAGEN CORP. WO200264793-A2. Homo sapiens. 15-NOV-2002 22-AUG-2002. ABS64723; RESULT 1 ABS64723

WPI; 2002-643487/69. P-PSDB; ABG32286.

New isolated G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer.

us-10-041-615-33.rng

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1021 TCAGAAACACCAAGTATCACCCCAGGCCAGAGGTTCTATGTTCTTAGCGGAGCACGTGGTC 1080
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601 GCCATTGGCTTCTGTGGGCCCAGTGGGGATCATCCTGTCCTGCTATATGAAGATCACCTGG
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P-PSDB; ADC86841.
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                                              This invention relates to a new isolated G-protein coupled receptor (GPCRX) polypeptide sequence and the cDNA encoding it. The GPCRX polypeptide sequence and the cDNA encoding it. The GPCRX nucleic acid and an antibody specific to the protein are useful for treating, preventing or alleviating a GPCRX-associated disorder is cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing and metabolic pathway modulation. The GPCRX polypeptide and mucleic acid are also useful for diagnosing the presence of or predisposition to a disease associated with altered levels of GPCRX, particularly cancer. The GPCRX nucleic acid and polypeptide are especially useful in the manufacture of a medicament for the arapeutic or prophylactic applications for disorders associated with aberrant GPCRX expression or activity, e.g. von Hippel-Lindau syndrome, arking a disease, stroke, tuberous sclerosis, hypercalcaemia, contained a disease, Huntington's disease, cerebral palsy, epilepsy, lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, disease, osteoporosis, inflammatory bowel disease, infertility, hyman syndrome, sclerosis, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman immundeficiency virus, auroimmune disease, infertility, hyman infertility, arking are turther used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and prove endicions of pharmacogenomics. The polypeptides can be used as immunderive medicine, and prove endicions of the polypeptides can be used as immunderive medicine, and prove endicions and as a substance of the polypeptides can be used as 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmacogenomics. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present sequence represents the CDNA encoding a human G protein coupled receptor related protein (GPCR) of the
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   Claim 9; Page 97; 252pp; English.
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                                                                                                                               The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the invention.
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                New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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Pred. No. 5.6e-176;
0; Mismatches 0; Indels 197; Gaps
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                                                                                               SEQ ID NO 1293; 28pp; English
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Best Local Similarity 83.6%;
Matches 1006; Conservative (
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                                 CAGGCCAGAGGTTCTATGTTCTTAGCGGAGCACGTGGTCTAACGTGTCATTTGCTTTATG
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 31289; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat discorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expression in a patient's genome that affect the activity of (1) by expressing inactive proteins or to polymucleotides may be used to produce the secreted (1), by inserting the purchain in host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to profess or diagnose and treat immune/haematopoietic-related diseases, especially cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic daride genomic cancer metastases of haematopoietic antigen genomic content the present invention. AAK54952 to AAK54950 and AAM82169

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The invention relates to human novel polymucleotides and associated polypeptides. The polymucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and responsation of neural brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral
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                                                      Sequence 9409 BP; 2123 A; 2163 C; 2259 G; 2864 T; 0 U; 0 Other;
                                                                                                                                                               Indels 197;
                                                                                                           Length 9409;
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represent sequences used in the exemplification of the
                                                                                                        Score 779; DB 4; L
Pred. No. 7.3e-176;
0; Mismatches 0;
                                                                                                             Query Match 70.6%;
Best Local Similarity 83.6%;
Matches 1006; Conservative
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1450 1041 1570 1510 1101 Human, gene; ss; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfasion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; 981 1511 CAGGCCAGAGGTTCTATGTGTTCTTAGCGGAGGACGTGGTCTAACGTGTCTATTGCTTTATG CAGGCCACCGTGGCCCTCATGAACATGAACTGTGGCATTACCCC-ATCATTTACTTCTTT CTTCAGAAACACCAAGTATCACC 1451 TCCTCCTCCTCCTCCTCCTCCACCCAGGAAAAGCTTCTTCAGAAAAACACCAAGTATCACC CAGGCCAGAGGTTCTATGTTCTTAGCGGAGCACGTGGTCTAACGTGTCATTTGCTTTATG GCATCCACCCATTACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCC á Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing. Wang Wang J, Asundi V, Zhou P, RT; ВЪ Liu C, Drmanac Human novel polynucleotide #33 ABK94922 standard; cDNA; 1526 30-NOV-2001; 2001WO-US047004. 30-NOV-2000; 2000US-00728952 (first entry) Tang YT, Goodrich RW, Yamazaki V, Ujwal ML,

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sclerosis. The sequences are involved in chemotactic or chemokinetic cativity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders eg. multiple solerosis and mysathenia gravis, allergic conditions used as asthma, thrombolysis or thrombosis and cosquiation disorders. Sequences ABK94890-ABK94982 represent human
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                  1261 IGCTGGTGGCCGTGGTGGTCTGCTTCAGCCCCTACCACCTCAACATCAAGAGTTCATGA
                                                                                                                       CGAGAGGGATGCTCCACCTGCCATCCTGTGCCGAGCGGAGGGCTTTCTTACTGTCCCTTC
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                                                                                                                                                                                                                                                   CATCCACCCATTACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCT
Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
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diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #14673.
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23-AUG-2000; 2000US-00649167.
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             involving aberrant protein expression or biological activity. The polypeptide and polyunclochide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce orher types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent din not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
(II). (I) and (II) are useful for treating disorders rotein expression or biological activity. The
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                                                                                                                                                                Sequence 1771 BP; 313 A; 531 C; 519 G; 407 T; 0 U; 1 Other;
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Pred. No. 1.8e-146;
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1679 1560 917 797 857 Alzheimer's disease; amyotrophic lateral scierosis, asthma; atherosclerosis, basal cell carcinoma; breast carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; chondrosarcoma; chondrosarcoma; carcinoma; depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; parkinson's disease; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberullosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; besity; diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy. Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis, The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the g protein-coupled (GPCR) polynuclocides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host cell comprising an expression vector comprising the GPCR sequence. 1621 cerreaggecacegregecercargaacargaacreregecarracec-arcarraacrr 1501 GCTGATGCTGGTGGCCGTGGTGGCTTCAGCCCCCTACCACCCCCAACATCAAGTT carceceacacacarecrecerecearecreses are considered and contract of the contract CCTTCAGGCCACCGTGGCCCTCATGAACATGAACTGTGGCCATTACCCCAATCATTTACTT CITIGCATCCACCATTACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTC CTGCTTCAGCCCCTACCACCTCAACATCAAGCAGTT CATGGCGAGGATGCTCCACCTGCCATCCTGTGCCGAGCGGAGGGCTTTCTTACTGTC ss; GAL4; galanin receptor; ä Pritchard Human DNA for potential G protein-coupled receptor #88 Fabre-Suver C, protein-coupled receptor; GPCR; ciccicciccicciccicciccicc 1740 CTCCTCCTCCTCCTCCTCCTCCTC 1764 (LIFE-) LIFESPAN BIOSCIENCES INC. Claim 2; Page 95; 144pp; English Burmer G, BP AAS98131 standard; cDNA; 1001 11-MAY-2000; 2000US-0203217P. 18-MAY-2000; 2000US-0205945P. 11-MAY-2001; 2001WO-US015332 (first entry) Miller M, WPI; 2002-066595/09. 40200185791-A1 Homo sapiens. 12-MAR-2002 LS-NOV-2001. Brown JP, AAS98131; 978 798 1561 828 918 738 RESULT 6 AAS98131/ 셤 à 쉼 셤 원 ઠ 셤 ઠે ठ

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antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the movel GPCR polypeptides of including the GAL4 polypeptide. The antibodies and nucleic acid probes as described above can be used to detect the presence of the polypeptides of an uncleic acids and are used to diagnose a variety of disease, of ascracis in which GPCRs are involved e.g., Alzheimer's disease, a myotrophic lateral sclerosis, asthma, atheroslerosis, basal cell carcinoma, breast carcinoma, acardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, Corbin's disease, depression, epilepsy, macular degeneration, lymphoma, melanoma, multiple sclerosis, rheumatoid arthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schoporosis, parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcration. The probes and antibodies are also useful for disagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene the invantion
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Sequence 1001 BP; 190 A; 315 C; 311 G; 185 T; 0 U; 0 Other;

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53.8%; Score 594.4; DB 6; Length 1001; llarity 98.7%; Pred. No. 4.7e-132; Conservative 0; Mismatches 6; Indels 2;
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Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia; attention deficit disorder; anxiety; depression; bipolar disorder; ss; neurological disorder; Huntington's disease; dementia; obesity; anorexia; metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis; type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer; cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser; antidepressant; anorectic; PCR primer; gene therapy.
                                                                                                                                                                                                                                  Human G Protein-Coupled Receptor (GPCR) cDNA #35.
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                                                      AAS42840 standard; cDNA; 536 BP
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23-FEB-2000; 2000US-0184303P.
23-FEB-2000; 2000US-0184304P.
23-FEB-2000; 2000US-0184305P.
23-FEB-2000; 2000US-0184397P.
03-MAR-2000; 2000US-0186457P.
03-MAR-2000; 2000US-0186810P.
03-MAR-2000; 2000US-01888064P.
03-APR-2000; 2000US-018880P.
03-APR-2000; 2000US-0134344P.
23-JUN-2000; 2000US-0134344P.
11-JUL-2000; 2000US-0213861P.
11-JUL-2000; 2000US-0213861P.
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20-JUL-2000; 2000US-0218492P
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New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity.

WPI; 2001-570628/64.

P-PSDB; AAU25588.

Claim 4; Page 82-83; 279pp; English.

Sequences AAS42996 FAAS42926 represent cDNA molecules and PCR primers for cDNA molecules encoding human G-protein coupled receptor (GPCR)

polypeptides. The protein and DNA sequences of the invention can be used to identify compounds which bind to GPCR polypeptides and in screening to identify compounds which bind to GPCR polypeptides and in screening or compounds that modulate GPCR activity. By screening a human subject for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, a GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as Huntington's disease, parkinson's disease and Tourette's syndrome, metabolic disorders such as pobesity, anorexia and type 2 diabetes, cardiovascular disorders such as thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis, viral infections caused by HIV and cancers

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Vogeli G,
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Sequence 536 BP; 93 A; 166 C; 182 G; 95 T; 0 U; 0 Other;
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protein-coupled receptors termed nGPCR-x nGPGR-x polynucleotides, polypeptides, and modulators may be used in the traatment of diseases and conditions such as viral infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, anorexia, hypotension, myocardial infarction.

Approxia, pretransion, myocardial infarction, obsity, anorexia, hypotension, and disease, and psychotic and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, manic depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. nGPCR-x polymucleotides and polypebtides, as well as nGPCR-x modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence encodes a G protein-coupled receptor of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding G protein-coupled receptors termed ndPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and schizophrenia).
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08-WAR-2000; 2000US-0187829F.
08-WAR-2000; 2000US-0187830F.
08-WAR-2000; 2000US-01878374F.
08-WAR-2000; 2000US-0187928F.
08-WAR-2000; 2000US-0187928F.
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08-WAR-2000; 2000US-018999F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity .... Matches 403; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-536778/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU19222
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nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the invention

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Brown JP, Miller M, Burmer G, Fabre-Suver C, Pritchard D;
                                       Human DNA for potential G protein-coupled receptor #68.
                                                                                                                                                                                                                         Claim 2; Page 83; 144pp; English.
                                                                                                                                                                   (LIFE-) LIFESPAN BIOSCIENCES INC.
         AAS98111 standard; DNA; 330 BP.
                                                                                                                                                   11-MAY-2000; 2000US-0203217P.
18-MAY-2000; 2000US-0205945P.
                                                                                                                                          11-MAY-2001; 2001WO-US015332.
                             12-MAR-2002 (first entry)
                                                                                                                                                                                      WPI; 2002-066595/09.
                                                                                                                      WO200185791-A1.
                                                                                                            Homo sapiens.
                                                                                                                                15-NOV-2001.
                   AAS98111;
                                                                                                                                                                                                               stroke.
RESULT 9
     AAS98111
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Sequence 330 BP; 46 A; 101 C; 108 G; 75 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sehan DP, Chalmers DT, Liaw CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA30635 standard; cDNA; 1086 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US023938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-329165/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY90630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antagonist; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA30635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCN) polymucleotides included in the specification. Also included are probes based on the GPCN sequences (including antisense probes), a host call comprising an expression vector comprising the GPCN sequence. The polypeptides are useful for antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCN polypeptides including the GAL4 polypeptide. The antibodies and nucleic acid probes as including the GAL4 polypeptide. The antibodies and nucleic acid probes as including the GAL4 polypeptide. The antibodies and nucleic acid such as used to detect the presence of the polypeptides and nucleic acids and are used to diagnose a variety of diseases or disorders in which GPCNs are involved e.g., Alzheimer's disease, arctinoma, breast carcinoma, sathma, atherocalerosis, basal cell carcinoma, breast carcinoma, actiony pathy, chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, depression, epilepsy, nactually degeneration, lymphome, melanoma, multiple sclerosis, is and many other disease listed in the Specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, pain perception classes else see is increase the expression of galanin receptor (GAL4) can the decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCN
                                                                                                                                                                                                                                                                                                                 Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basel cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; parkinson's disease; psoriasis; rhemmatod; arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; osteostar, diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
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                                                                                                                                          349 GGGGTCTACCTCATGGCCTGTGTGAGCGTGGACCATTACCCAGCTGTGGTCTGTGCCCAC 408
                                                                                                                                                                                                                                                                                    468
                                                                                                                                                                                                                                                                                                                                               61 reseccicececercecarescrescresceaeceaecrascrascrascearescearereseaec 120
                                                                                                                                                                                                                                                                                                                                                                                                                      528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 CTGGIGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTGTCCTGCTATATG 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 credicecerrieccarrecerrencesceaereses 300
                                                                                                                                                                                                  1 GGGGTCTACCTCATGGCCTGTGTGTGAGCGTGGACCATTACCCAGCTGTGTCTGTGTCTCCCAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to constitutively active, non-endogenous versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist;
                                                                                                                                                                                                                                                                            469 TTGGTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TIGGIGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 AAGCTGGCCTGCATGGAGTACAGCAGCATGAGTCAGTCCTCGGGGCTGCCCCTCATGGTC
                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
       Length 330;
   Query Match 29.7%; Score 328.4; DB 6; Length 3 Best Local Similarity 99.7%; Pred. No. 1.3e-68; Matches 329; Conservative 0; Mismatches 1; Indels
DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AAGATCACCTGGAAGCTGGGCAGCACAGCT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649 AAGATCACCTGGAAGCTGTGCAGCACAGCT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G protein-coupled receptor EBI2 cDNA.
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of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY906377 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743) and to DNA encoding them (AAA30709-A30743). The mutant proteins of the invention contain a mutation in a portion of the proteins of the invention contain a (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, cis substituted for an endogenous residue in TM6 to form a sequence X-CC (AA)15-pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys, when the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be condensed in a pagnists or a mixture of endogenous and non-endogenous, cor a mixture of endogenous and non-endogenous corrections are also useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agonists and partial agonists for use as pharmaceutical capturicular Appendix or the normal and diseases and discoders associated with that receptors in normal and diseases and discoders associated with that receptors because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence compounds without the need for endogenous ligands. The present sequence represents cDNA encoding a human wild-type GPCR used in an exemplification of the invention. This was cloned and subjected to site-off invention. This was cloned and subjected to site-off invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant of the invention
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Sequence 1086 BP; 314 A; 242 C; 206 G; 324 T; 0 U; 0 Other;

640 160 280 340 343 400 460 463 520 523 580 583 643 700 703 GGAAAGGACGCCACTGGCTGCCTTACGCTGCTGATGCTGGTGGCCGTGGTGG 760 163 TTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCTG 220 223 283 403 CTCTGTTCTACACACCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGCC 104 CTCTGCATTACAGCCTCGTCTTCATCATTGGCTCGTGGGAAACTTACTAGCCTTGGTCG 164 icarrericadadedegadadadreneracedecereraredadadrea 284 TIGACIGGAGAATCGGAGATGCCTIGIGTAGGATAACTGCGCTAGTGTTTTACATCAACA CCTACGGGGGGGTCTACCTCATGGCCTGTGTGAGCGTGGACCATTACCCAGCTGTGGTCT GTGCCCACTGGGGCCCCGCGCCTCCGCACGCTGGCCAGGCTGGTCTGCGTGGCCA ACCCTCTACGCTACAACAAGATAAAAGGATTGAACATGCAAAAGGCGTGTGCATATTTG TCTGGACCTTGGTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGC reregarreragrarrecreadaenereceaerecreareaaeerragraaaeeage TCATGGTCCTGGTGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTGTCCT GCTATATGAAGATCACCTGGAAGCTGTGCAGCACAGCTCGGGAGGACCCAGTGACCAGCA 224 TITICIGATATACITITITACCACGCTTTGCCTACACGAATAGCCTACTATGCAATGGGCT CCAGCTGGCCTTTCGGCAAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCGACA ggaircrigcirriggggargrundaragarargracriccacritaraarcarcricarcri 221 TGTCTGACCTGCTGTTCACCGTGGCCTTACCGGGAAGGGTGGTGTTATGTGTGCTGGCT Gaps 9 DB 3; Length 1086; Score 184.8; DB 3; Length Pred. No. 4.1e-34; 0; Mismatches 457; Indels 16.7%; 50.6%; al Similarity 50.6 475; Conservative Query Match Best Local Si Matches 475 524 344 404 464 581 584 701 161 281 341 401 461 521 641 644 101 g g g ઠે 셤 중 염 챵 8 요 요 g qq 엺 ઠે ò ઠે g 8 ò

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944 ATAAGAGAAAGGTTATGAGGATGCTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTG 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; EBI2; G-protein coupled receptor; receptor; neuropeptide; corticotropin releasing factor; antidepressant; tranquillizer; nootropic; neuroprotective; cerebroprotective; antiinflammatory; antirheumatic; antiarthritic; anorectic; gene; 88.
                                                                                                                                823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimetic, as ligand
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                                                                                                                                                                                                                                                                    CTAATTTCCTGGAATGTAGCCAAAGACATTCGTTCCAGATTTCTCTGCACTTTACAGTAT
                                                                                                                                                                                                    821 TGCCATCC-----TGTGCCGAGCGGAGGGCTTTCTTACTGTCCCTTCAGGCCACCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                    884 GCC1GA1GAACT1CAAT1GCTGCA1GGACCCTT1TA1C1ACT1CTT1GCA1GTAAAGGGT
                                                                TCTGCTTCAGCCCCTACCACCTCAACATCAAGCAGTTCATGGCGAGAGGGATGCTCCACC
                                                                                                                                                                                                                                                                                                                                    CCCTCATGAACATGAACTGTGGCATTACCCCAATCATTTACTTTGCATCCACCCATT
704 AATCIGGIGIAAACAAAAGGCICICAACAATIAITAITCIIAITAITGITGITITITIC
                                                                                                                            764 rererricaeaeerracearerracaarrarreaearararaaaaaeerreerere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G-protein coupled receptor EBI2 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1004 TGAAGÍCAGCCCTGAAGÁAATÍCACGTGAÁATGACA 1041
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1. .1086
/*tag= a
/product= "Human EBIZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC48996 standard; cDNA; 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-2001; 2001GB-00019920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABR42051
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also provides screening methods to identify agonists and antagonists for EBI2. Modulators of the receptor may find use in diagnosing or treating depression, anxiety-related discorders (e.g. panic), stress, Alzheimer's disease, stroke, inflammatory disorders (e.g. rheumatorid atthritis), eating disorders (e.g. anorexia) and obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 CCAGCTGGCCTTTCGGCAAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCGACA
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16.7%; Score 184.8; DB 7; Length 1086;
Best Local Similarity 50.6%; Pred. No. 4.1e-34;
Matches 475; Conservative 0; Mismatches 457; Indels 6;
                                                                                                                                                                                                               Sequence 1086 BP; 314 A; 242 C; 206 G; 324 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCTCCACCCCAGGAAAGCTTCTTCAGAACACCCA 1032
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled constitutively active version of an endogenous human G protein-coupled intracellular-3 (IC3) region, by substituting a specific anino acid in tracellular-3 (IC3) region, by substituting a specific anino acid in tracellular-3 (IC3) region and an intracellular loop 3 region. The altered human GPCR cegion and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may be used to create a transgenic animal expressing the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds the method allows screening for compounds the method allows screening for compounds the method allows for this is particularly useful in allowing currently known. This sequence represents for which no ligand is currently known. This sequence represents contain a human GPCR polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 CTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGCC 160
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Pred. No. 4.1e-34;
0; Mismatches 457; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1086 BP; 314 A; 242 C; 206 G; 324 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                Human; gene; ss; G protein-coupled receptor; GPCR;
transmembrane-6 region; TM6; intracellular-3 region; IC3.
1004 TGAAGTCAGCCCCTGAAGAAAATTCACGTGAAATGACA 1041
                                                                                                                                                                                                                               Human G protein-coupled receptor cDNA #22.
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                                                                                                                ADC22596 standard; cDNA; 1086
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98US-00060188.
98US-0090783P.
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al Similarity 50.6%;
475; Conservative
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Matches 475; Conserv
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                                                                                                                                                       ADC22596;
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Epstein Barr virus; EBV; induction; detection; diagnosis; lymphocytes; antigen; growth; differentiation; mediator; infectious mononucleosis;
                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in enlarging, increasing RNA synthesis, expressing activation antigens and adhesion molecules, secreting IG and proliferating. Unlike antigens stimulated B lymphocytes, EBV infected B lymphocytes continue to proliferate (in vitro) as immortalised lymphocytes continue to of the similar effects of EBV and antigen, EBV induced genes are likely to include mediators of antigen induced B lymphocyte growth or differentiation. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s) and antibodies to EBI1, 2 and 3 - useful for detecting EBV by hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccraceagagagreracererargecerargagegregacearraceagererer
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Location/Qualifiers
34. :1119
/*trag= a
/product= "Epstein Barr virus induced polypeptide.
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16.7%; Score 184.8; DB 2; Length 1643;
Best Local Similarity 50.6%; Pred. No. 4.8e-34;
Matches 475; Conservative 0; Mismatches 457; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1643 BP; 509 A; 339 C; 285 G; 510 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 56-58; 84pp; English
                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                          93WO-US009636
                                                                                                                                                                                                                                                                         92US-00980518
                                                                                                                                                                                                                                                                                                                                                                       Birkenbach M, Kieff E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or by immunoassay
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                                                                                                                                                                                                                          08-OCT-1993;
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                                                                                                                                                                         09-JUN-1994.
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Epstein Barr virus induced (EBI-2) gene

(revised)
(first entry)

25-MAR-2003 03-FEB-1995 AAQ64126;

1643

AAQ64126 standard;

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977 ATAAGAGAAAGGTTATGAGGATGCTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTG 1036
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                                                                                                                                                                                                                                                                                                                                           875 CCTCATGAACATGAACTGTGGCATTACCCCAATCATTTACTTCTTTGCATCCACCCATT 934
                                                                                                                                                                                                                                                                                                                                                               917 GCCTGATGAACTTCCAATTGCTGCATGGACCCTTTTATCTACTTCTTTGCATGTAAGGGT 976
                                                                                                                                                                                                                                                                                                                                                                                                    935 ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGCTCTTCCTCCTCCTCCTCCTCCT
                                                                                                              GCTATATGAAGATCACCTGGAAGCTGTGCAGCACAGCTCGGGAGGACCCAGTGACCAGCA
                                                                                                                                                                    701 GGAAAGGACGCCACTGGCGAGGCTGCTTACGCTGCTGATGGTGGTGGCGTGGTGG
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                                                                                                                                                                                                                                                                                   821 TGCCATCC-----TGTGCCGAGCGGAGGCTTTCTTACTGTCCTTCAGGCCACCGTGG
                                                       581 TCATGGTCCTGGTGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTGTCCT
                                                                                   617 GGAITCTGCTTGGGGCCAIGITTCATAGGATATGTACTTCCACTTATAATCATTCTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessing; monitoring; foetal development; placental development; Epstein Barr virus; EBV; induced gene 2; EBI-2; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           995 CCTCCTCCACCCCAGGAAAGCTTCTTCAGAAACACCA 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA for Epstein Barr virus induced gene 2 (EBI-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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94US-00352678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-271060/24.
P-PSDB; AAW53623.
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                                                                                                                 The present sequence was used in the development of a novel method for assessing or monitoring foetal or placental development. The method comprises taking a maternal serum sample, and detecting the level or size of Epstein Barr virus (EBV) induced gene or protein 3 (EBI-3) to obtain a result, which can be compared to a control to assess or monitor foetal or placental development
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Assessing or monitoring foetal or placental development - comprises detecting the level or size of Epstein Barr virus induced nucleic acid protein in maternal serum samples.
                                                                                                                                                                                                                                                                                                                                                                                   CTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGCC
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                                                                                                                                                                                                                                                                                                 Query Match
16.7%; Score 184.8; DB 2; Length 1643;
Best Local Similarity 50.6%; Pred. No. 4.8e-34;
Matches 475; Conservative 0; Mismatches 457; Indels 6;
                                                                                                                                                                                                                                                              Sequence 1643 BP; 509 A; 339 C; 285 G; 510 T; 0 U; 0 Other;
                                                                                Example 2; Col 43-46; 45pp; English.
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The invention relates to a combination which, comprises a number of polymucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polymucleotides. The microarray is particularly useful in the diagnostics and treatment of cancer and immunopathology and neuropathology. The microarray is useful in the discovery and development, toxicological and carcinogenicity studies, of secovery and development, toxicological and carcinogenicity studies, is consistently progression of diseases in carcinogenicity studies, profiles for the effects of currently available therapeutic drugs. The molitoring progression of diseases of profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of genes coling array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AlDS and asthama, neuropathies e.g. Alzheimer's disease and parkinson's disease. The present sequence are persents a polymucleotide form part of the printed specification but was obtained in electronic form part directly from USPPO at the contact of the printed specification but was obtained in electronic forms.
                                                                                    977 ATAAGAGAAAGGTTATGAGGATGCTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTG 1036
                                           ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCT 994
GCCTGAIGAACTTCAATTGCTGCATGGACCCTTTTATCTACTTCTTTGCATGTAAAGGGT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; probe; ss; array element; Parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                              Human signalling pathway polynucleotide probe SEQ ID NO 1279
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                                                                                                                             995 CCTCCTCCACCCCAGGAAAGCTTCTTCAGAAACACCA 1032
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Best Local Similarity 50.6%; Pred. No. 4.8e-34;
Matches 475; Conservative 0; Mismatches 457;
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Search completed: February 21, 2004, 19:27:06 Job time : 494 secs

Score 184.8; DB 7; Length 1643,

16.7%;

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GenCore version 5.1.6

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CM nucleic - nucleic search, using sw model

Run on: February 21, 2004, 19:12:09; Search time 110 Seconds

(without alignments)

5569.689 Million cell updates/sec

Title: US-10-041-615-33

Perfect score: 1104

Sequence: 1104

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-brocessing: Minimum Match 0*

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Listued Parents NA:*

| cgn2 6/ptodata/2/ina/5A COMB.seq:*
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| cgn2 6/ptodata/2/ina/6A COMB.seq:*
| cgn2 6/ptodata/2/ina/6B COMB.seq:*
| cgn2 6/ptodata/2/ina/BCOMB.seq:*
| cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
| cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
→	84.	16.7	108	4	-09-17	Sequence 77, Appl
2	184.8	16.7	164	ч	US~08-383-750-3	Sequence 3, Appli
m	84.	16.7	164	ო	-678-	equence 3,
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ស	84.	16.7	164	4		127
9	84.	16.7	1643	Ŋ	PCT-US93-09636-3	equence
7	183.2	16.6	rd	4	US-09-170-496D-205	Sequence 205, App
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თ	112	10.1	1020	4	0	equence
10	112	10.1	1020	4	-	181
11	112	10.1	7	4	US-09-016-434-1484	148
12	112	10.1		н	0	43, 7
13	112	10.1	1901	m	US-09-299-843A-43	43
14	112	10,1	1901	4	US-09-088-337B-43	43,
15	112	10.1	1901	ß	PCT-US93-11153-43	43
16	112	10.1	~	ហ	PCT-US95-07180-1	7
17	106.8	7.6	N	4	39-21	'n
18	106.8	•	7	4	38-432-174A	1
19	106.8		CA	m	US-08-147-592A-3	m
20	106.8	•	~	4	08-29	'n
21	105.4	9.5	Н	4	US-08-148-708-3	m
22	105.4		Н	Н	18-759	ď
23	105.4	9.5	Н	4	US-08-148-708-6	ဖ
24	105.4	•	7	4	09-016	H
25	105.4	9.5	Н	ហ	PCT-US95-09383-2	2, App
26	105.2	٠	7	N	98-	H
27	105.2	9.5	-	m	US-08-387-707-7	Sequence 7, Appli

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-08-405-271A-7 US-09-170-496D-117	US-09-170-496D-225	US-09-034-985-1	US-08-724-974A-1	US-09-364-425B-26	US-08-442-134A-1	US-08-444-581B-1	US-08-446-088A-1	US-08-432-174A-3	US-09-576-160B-9	US-09-016-434-1405	US-09-576-160B-12	US-08-405-271A-18	US-09-016-434-1391	US-09-023-655-1417	US-09-976-594-171	US-09-170-496D-3
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ALIGNMENTS

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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 16.7%; Score 184.8; DB 4; Length 1086; Local Similarity 50.6%; Pred. No. 3.4e-36; les 475; Conservative 0; Mismatches 457; Indels 6;
                                               Sequence 77, Application US/09170496D; Patent No. 6555339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                / TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-170-496D-77
RESULT 1
US-09-170-496D-77
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 77
LENGTH: 1086
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935 ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCT 994
    INFORMATION FOR SEQ ID NO: 3:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                   CDS
34..1116
                                                                                                            TOPOLOGY: linear
                                                                                                                                               , NAME/KEY;
, LOCATION;
US-08-383-750-3
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464 TCTGGATTCTAGTATTTGCTCAGACTCCCACTCCTCATCAACCCTATGTCAAAGCAGG 523
                                                              524 AGGCTGAAAGGATTACATGCATGGAGTATCCAAACTTTGAAGAAACTAAATCTCTTCCCT 583
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Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: U.S.A.
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ZIP: U.S.A.
ZIP: U.S.A.
ZIP: U.S.A.
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAECHIIR Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: POX. Samuel, L.
REGISTRATION WUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 CCTACGGGGGGTCTACCTCATGGCCTGTGTGAGCGTGGACCATTACCCAGCTGTGGTCT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 ACCCTCTACGCTACAACAAGATAAAAAGGATTGAACATGCAAAAGGCGTGTGCATATTTG 496
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tch 16.7%; Score 184.8; DB 1; Length 1643; al Similarity 50.6%; Pred. No. 4e-36; 475; Conservative 0; Mismatches 457; Indels 6;
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700 736 760 196 820 856

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377 carardcadgrefreaacritatidaccredacratreaccerreatrecretecated
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GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Rieff, Elliott
ITIE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GEN
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: WA
COUNTY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,954
                                           341 CCTACGGGGGGGTCTACCTCATGGCCT
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Patent No. 6500926
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977 ATAAGAGAAAGGTTATGAGGATGCTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTG 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Biliott
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOUTHWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INPORMATION:
NAME: Gates Edward R: 31,616
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
REFERENCE/POCKET NUMBER: 31,616
REGISCOMMULICATION INFORMATION:
TELLECOMMULICATION INFORMATION:
                                                                                                CCTCCTCCACCCCAGGAAAGCTTCTTCAGAAACACCA 1032
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Pred. No. 4e-36;
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600 Atlantic Avenue
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Best Local Similarity 50.6%;
Matches 475; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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LOCATION:
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101 CICTGITCIACACACCCCICCIGGICTICAGIGCCCIGGGAAACAICCITGCCCTITGCC 160
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3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-016-434-1279
; Sequence 1279, Application US/09016434
Patent No. 6500938
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERNCE/OCKET NUMBER: PA-0
TELECOMMUNICATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1279:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: GENBANK
; CLONE: 9292056
US-09-016-434-1279
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IMMEDIATE SOURCE:
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                                                                                                                                                                            B0801/7044
FILING DATE:
CLASSIFICATION
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gate, Edward R.
REGISTRATION NUMBER: 31 616
REGISTRATION NUMBER: B091/7
TELEPRONE: 617-720-3500
TELEPRAK: 617-720-3501
TELEPRAK: 617-720-341
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: mucleic acid
STRANDEDENESS: double
TOPPCLOGY: linear
MOLECULE TYPE: CDNA
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LOCATION: 34..1116
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Matches 475;
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977 ATAAGAGAAAGGTTATGAGGATGCTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTG 1036
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875 CCCTCATGAACATGAACTGTGGCATTACCCCAATCATTTACTTCTTTGCATCCACCATT 934
                                                                                                                                                                                                                                                                                                                                                                                                                         935 ACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCTT 994
                                                                                                                      821 TGCCATCC-----TGTGCCGAGCGGAGGGCTTTCTTACTGTCCCTTCAGGCCACCGTGG 874
                                                                                                                                                                                                857 CTAATTTCCTGGAATGTAGCCAAAGACATTCGTTCCAGATTTCTCTGCACTTTACAGTAT 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.7%; Score 184.8; DB 4; Length 1643;
Best Local Similarity 50.6%; Pred. No. 4e-36;
Matches 475; Conservative 0; Mismatches 457; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Word berfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             995 CCTCCTCCACCCCAGGAAAGCTTCTTCAGAACACCCA 1032
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COUNTRY: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:

Washington

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs

nucleic acid

TOPOLOGY: linear TYPE: nucle: STRANDEDNESS

CDS 34..1116

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977 Araagagarangarangagangcigaaacggcaagrcagigraricgarrictagggcig 1036
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CHCTGCATTACAGCCTCGTCTTCATCATTGGCTCGTGGGAAACTTACTAGCCTTGGTCG 196
                                                         TTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCTG 220
                                                                                            rcarrenteaaaacaggaaaaaacrecaccececerareacaaarregga 256
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                                                                              8; DB 5; Length 1643; 4e-36;
                                                                                                                    0; Mismatches 457; Indels
                                                                              Score 184.8;
Pred. No. 4e-
                                                                            16.7%;
50.6%;
                                                                                 Query Match
Best Local Similarity 50.6
Matches 475; Conservative
, NAME/KEY:
, LOCATION:
PCT-US93-09636-3
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RESULT 6
PCT-US93-09636-3
; Sequence 3, Application PC/TUS9309636
; Sequence 3, Application PC/TUS9309636
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

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US-09-016-434-1482

US-09-016-434-1482

| Sequence 1482, Application US/09016434
| Patent No. 6500938
| GENERAL INFORMATION: GAPLICANT: Jainice Au-Young APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGN TITLE OF INVENTION: PATHWAY GENE EXPRESSION NUMBER OF SEQUENCES: 1490
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 FORTER DRIVE
| COUNTRY: USA COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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APPLICATION NUMBER: US/09/016,434
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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Sequence 205, Application US/09170496D
Sequence 205, Application US/09170496D
Sequence 205, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Chalmers. Derek T.
APPLICANT: Chalmers. Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 205
LENGTH: 1086
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Pred, No. 8.5e-20
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                                                                                                                                            PA-0002
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00C
TELECOMUNICATION INFORMATION:
TELEPAX: (650) 845-0555
TELEPAX: (650) 845-04166
INFORMATION FOR SEQ ID NO: 1482:
SEQUENCE CHARACTERISTICS:
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48.1%;
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Best Local Similarity 48.1
Matches 399; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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; CLONE: 9984506
US-09-016-434-1482
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Sequence 31, Application US/09170496D
Sequence 31, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 19/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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Pred, No. 2.8e-18;
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CORGANISM: Homo sapiens
US-09-170-496D-31
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US-09-170-496D-31
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APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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Pred. No. 3.5e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1484, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,0
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-09-016-434-1484
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Parent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
                                                                                                                                                                                                                                                                       CCCTTCAGGCCACCGTGGCCCTCATGAACAGTGTGGCATTACCCCAATCATTTACT 916
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Pred. No. 2.8e-18;
0; Mismatches 375; Indels 2
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CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 181
LENGTH: 1020
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Matches 384; Conservative
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CORGANISM: Homo sapiens
US-09-170-496D-181
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US-09-170-496D-181
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1260 AGAAGGC------CTCCCACCATGCCCTGGTGTCCCTGGCAGTGGCCTTCACCT 1307
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CDIAL
STATE: 11.1.

COUNTRY: USA

ZIP: 60666

COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: PAPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 31.30
ATTORNEY/AGENT INFORMATION:
NAME: NO. 575804404
TELEFRAX: (312) 474-648
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Pred. No. 3.5e-18;
0; Mismatches 375;
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Best Local Similarity 48.9
Matches 384; Conservative
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Patent No. 5759804
GENERAL INPORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                     Matches 384; Conservative
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US-08-153-848-43
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1308 TCCCGTTCATCACCACGTCACCTGCTACCTGCTGATCATCACCAGCGCAGGGCC 1367
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Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE: ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
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REGISTRATION UNIBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR PAPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-UN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
ATTORNEY/AGENT INFORMATION:
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WEDIUM TYPE: Floppy disk
CMEDIUM TIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
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CITY: Chicago
STATE: Illinois
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US-09-299-843A-43
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1260 AGAAGGC------CTCCCACCATGCCCTGGTGTCCCTGGGCAGTGGCCTTCACCT 1307
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                                                                                                                                                                              10.1%; Score 112; DB 3; Length 1901;
48.9%; Pred. no. 3.5e-18;
tive 0; Mismatches 375; Indels 27; Gaps
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; Sequence 43, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                             Matches 384; Conservative
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                                                                                                                                                                              Query Match
Best Local Similarity
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TOPOLOGY: linear
                                                                          ) NAME/KEY: CDS
) LOCATION: 701.
US-09-299-843A-43
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617 GGCCAGTGGGGATCATCCTGTTGTATGAAGATCACCTGGAAGCTGTGCAGCACCAG 676
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GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: NOVEL 1.
TITLE OF INVENTION: NOVEL Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marball, O'Toole, Gerstein, Murray &
ADDRESSEE: Marball, O'Toole, Gerstein, Murray &
CITY: Chicago
STREET: Glob Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 07/977,452
PILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 CGGCGTTTGTGCTCTACACCGACACCTACGGGGGGGTCTACCTCATGGCCTGTGAGCG
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                                                                                Gray, Patrick W. Schwelkart, Vicki L. Schwelkart, Vicki L. TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
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Best Local Similarity 48.9%; Pred. No. 3.5e-18;
Matches 384; Conservative 0; Mismatches 375; Indels
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOC TOOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILLING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILLING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6346574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
REPLICATION UNDRES: US/09/088,3378
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-09-088-337B-43
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TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1901 base pairs
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STRANDEDNESS: single
                                          APPLICANT: Godiska, Ronald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinoi
COUNTRY: USA
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10.1%; Score 112; DB 5; Length 1901;
Best Local Similarity 48.9%; Pred. No. 3.5e-18;
Matches 384; Conservative 0; Mismatches 375; Indelf 27; Gaps
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INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
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PCT-US93-11153-43
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Search completed: February 21, 2004, 21:28:25 Job time : 115 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 33, Appl	Sequence 1619, Ap	Sequence 1293, Ap	Sequence 40, Appl	Sequence 35, Appl	Sequence 64, Appl	Sequence 1, Appli	Sequence 77, Appl	Sequence 1279, Ap	Sequence 39, Appl	Sequence 205, App	Sequence 111, App	Sequence 29, Appl	Sequence 90, Appl	Sequence 10498, A
ΠD	US-10-041-615-33	US-10-017-161-1619	US-10-292-798-1293	US-09-728-952-40	US-09-791-932-35	US-09-801-944B-64	US-10-222-024-1	US-10-251-385-77	US-10-305-720-1279	US-10-247-671-39	US-10-251-385-205	US-10-225-567A-111	US-10-350-923B-29	US-09-812-102-90	US-09-918-995-10498
	15	4	12	σ	10	T	14	14	13	14	14	14	15	σ	10
, Query Match Length DB	1104	4319	4319	1526	536	556	1086	1086	1643	2477	1086	1638	1556	594	548
Query Match	100.0	70.6	70.6	6.09	36.0	34.3	16.7	16.7	16.7	16.7	16.6	16.6	15.6	13.4	11.2
Score	1104	779	779	672.8	397.2	378.4	184.8	184.8	184.8	184.8	183.2	183.2	172.2	148	123.4
Result No.		7	m	4	Ŋ	φ U	7	80	o,	10	11	. 12	13	14	. 15

Sequence 3, Appli	20	21	72	Sequence 1482, Ap		Sequence 3, Appli	Sequence 5, Appli			Sequence 181, App		Sequence 303, App	Sequence 1, Appli	Sequence 707, App	Sequence 619, App	1, 7	w	ຕັ	1, Ar	Sequence 844, App	462,	112	11,	563	Sequence 565, App	567	Sednence 850, App	e 47	Sequence 7, Appli
US-10-023-586B-3	US-10-333-946-20	US-10-225-567A-216	US-10-101-510-722	. US-10-305-720-1482	US-10-101-510-431	US-09-885-453-3	US-10-079-384-5	US-09-788-133-1	US-10-251-385-31	. US-10-251-385-181	: US-10-305-720-1484	. US-10-225-567A-303	US-10-023-586B-1	US-10-017-161-707	. US-10-292-798-619	US-10-275-910-1	US-10-088-726-25	US-09-214-904-3	US-10-112-599A-1	US-10-005-956-844	. US-09-826-509-462	S US-10-305-720-1123	US-10-005-956-11	t US-10-005-956-563	L US-10-005-956-565	1 US-10-005-956-567	1 US-10-005-956-850	1 US-10-225-567A-47	US-09-823-114-7
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102	107	202	202	202	211	101	101	102	102	1020	190	207	108	133	133	314	100	221	221	373	117	137	373	373	373	373	373	373	182
10.8	10.8	10.7	10.7	10.7	10.6	10.4	10.4	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.0	9.7	7.6	9.6	9.5	9.5	9	9.0	9	9.5	ο. Ω.	9.5	9.5
119.4	119.4	118.6	118.6	118.6	117	115	115	112	112	112	112	112	111.8	111.8	111.8	111.8	110.2	106.8	106.8	106	105.4	105.4	105.4	105.4	105.4	105.4	105.4	105.4	105.2
16	17	18	19	20	21	22	23	24	25	5 6	27	28	29	30	31	32	33	3.4	S	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-10-01-615-33

US-10-01-615-33

Sequence 33, Application US/10041615

Sequence 33, Application US/10041615

Sequence 33, Application US/20040014038A1

SEQUENCE 31, ENGRENCE 51

APPLICANT: Edinger, Shlomit R

APPLICANT: Edinger, Shlomit R

APPLICANT: Enternan, Karen

APPLICANT: Smithson, Glennan

APPLICANT: Relation UNIVERS.

CURRENT RELNG DATE: 20040014038A1e1 GPCR-Like Proteins and Nucleic Acids Encoding TILE OF INVENTION: No. US20040014038A1e1 GPCR-Like Proteins and Nucleic Acids Encoding DATE: 2010-01-03

CURRENT APPLICATION NUMBER: 60/259,552

PRIOR PAPLICATION NUMBER: 60/259,552

PRIOR PAPLICANTON NUMBER: 60/259,552

PRIOR PAPLICANTON NUMBER: 60/259,552

PRIOR PILING DATE: 2001-01-03

SEQUENCE CONTRACT: 2001-01-03

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 33

LENGTH: 1104

TYPE: DNA

ORGANISM: Homo sapiens

PEARLY MATCH

PEARLY CONTRACT: CDS

US-10-041-615-33

Query Match

Best Local Similarity 100.0%; Pred. No. 2.6e-310; Indels 0; Gaps 0;
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                                                                                                                                                                                                                                                                                                                                                                                              CIGGICTICAGAGCCCTGGGAAACATCCTTGCCTTTGCCTTACCTGCAAAAGAGCAGG 180
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Sequence 1619, Application US/10017161

Publication No. US20000143668A1

Publication No. US20000143668A1

GENERAL INFORMATION

APPLICANT: SUAL, MIXIKO

APPLICANT: ANTIMAM, YUTARA

APPLICANT: ANTIMAM, YUTARA

APPLICANT: ANTIMAM, YUTARA

APPLICANT: ANTIMAM, YUTARA

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0122

CURRENT APPLICATION NUMBER: UP 2001/246789

FRIOR PEDITOR TILING DATE: 2002-12-18

FRIOR PEDITOR NOWE: 18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PATENTING VET: 2.1

SEQ ID NO 1619

LENGTH: 4319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: modified base

; LOCATION: (1)..(48)

; CTHER INFORMATION: a, t, c, g, unknown or other

US-10-017-161-1619
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LOCATION: (3660)..(4119)
FEATURE:
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LOCATION: (3128)..(3531)
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (201)..(308)
FEATURE:
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NAME/KEY: SOURCE
LOCATION: (1)..(4319)
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1539 GCGGGAAAGGACACCACCGGCGGGCAGCCCAGGAGGACCCAGTGACCAACAGGAAAGGA 3598
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Pred. No. 1.6e-215;
0; Mismatches 0;
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                                                                                                                                                                            | FEATURE: | COCATION: Source | FEATURE: | LOCATION: Source | FEATURE: | LOCATION: (1) ... (4319) | FEATURE: | NAME/KEY: CDS | LOCATION: (201) ... (308) | FEATURE: | NAME/KEY: CDS | LOCATION: (3128) ... (3531) | FEATURE: | LOCATION: (3660) ... (4119) | FEATURE: | NAME/KEY: CDS | LOCATION: (3660) ... (4119) | FEATURE: | NAME/KEY: modified base | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (1) ... (48) | LOCATION: (2) ... (4119) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (4) ... (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) | LOCATION: (48) 
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Best Local Similarity 83.6%;
Matches 1006; Conservative
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFWARE: PatentIn Ver. 2.1
SEQ ID NO 1293
LENGTH: 4319
                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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Publication No. US20030235833A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUNA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANCSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REPREMENCE: 08435/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT RILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
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                              3479 recrecrarardaacarcaccrecaaccrecrecaccaccaccaccacacacccacacca 3538
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                                                                                                               CCCCTCATGGTCCTGGTGGCCTTTGCCCATTGGCTTCTGTGGGGCCCAGTGGGGATCATCCTG
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Query Match 60.9%; Score 672.8; DB 9; Length 1526; Best Local Similarity 81.9%; Pred. No. 7.3e-185; Matches 901; Conservative 0; Mismatches 2; Indels 197; Gaps 3;	cccrccreercrrcereccr 	OY 158 GCCTTACCTGTCAAAAGACCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGG 217					QY 458 CCATCTGGACCTTGCTGCTGCTGCTGCTTGCTCTTGATGCCCATGACCAAGC 517	Oy 518 CGCTGGTGGGCAAGCTGCATGGAGTACAGCAGCAGGTCCTCGGGCTGC 577	Qy 578 CCCTGATGGTCCTGGTGCCTTTGCCATTGGCGATCGGGCCGGTGGGGCAGTGGGGATCATCTGT 637	638	Db 961 CCTGCTATATGAAGATCACCTGGAAGCTGTGGAGCTGGGAAGACCTGGAGCTGGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGAGAAGCTGGGAAGAAGCTGGAGAAGCTGGGAAGAAGCTGGGAAGAAGCTGGAGAAGCTGGGAAGAAGCTGGAGAAGCTGGGAAGAAGCTGGAAGAAGCTGGAAGAAGCTGGAAGAAGCTGGAAGAAGCTGGAAGAAGCTGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	Qy 679	679	Db 1081 GCCACCGGCGGGCAGCCCAGGAGCCCAGTGACCAGGGGGAAAGGACACCACCAGCAG 1140		1141	Db 1201 AGGACCCAGTGACAGGAAAGGACGCCACTGGCGACTGCCTGC	Δy 743 IGCIGGIGGCGIGGTGGTCGTTTGAGCCCCTACCACCTCAAGCAGTCAAGCAGTTCATGG 802	803			
67	20090A	0000000 010010	d:	802 GCGAGAGGATGCTCCCATCCTGTGCCCCTACCACCTCCACACACA	9839 GCGAGAGGGATGCTCCACCTGCCATCCTGTGCCGAGCGCATTACTTAC	3899 CAGGCCACCGTGGCCCTCATGAACATGAACTGTGGGCATTTAAAGCCTCAATACATTTCTTCTCCTCC 922 GCATCCACCCATTACAGGAAATGGCTCCTGGGCATTTTAAAGCTCTCAAAGGGTCTTCCTCC	982 TCCTCCTCCTCCTCCAGGGAAAAGCTTCTTCAGAAACACCAAGTATCACCCAGGAAACACCAAGTATCACCCAGGAAAAACACTTCTTCAGAAAACACCAAGTATCACCCAGGAAAAACACTTCTTCAGAAAACACAAAATCACCCAGGAAAAAAAA	TITAIG	Db 4078 CAGGCCAGAGGTTCTATGTTCTTAGCGGAGCACGTGGTCTAACGTGTCATTTGCTTTATG 4137 Qy 1102 ACT 1104	Db 4138 ACT 4140	RESULT 4		GENERAL INFORMATION: APPLICANT: Tang, Y. Tom abplicant: Zhon, Ping		APPLICANT: Asundi, Vinod APPLICANT: Wang, Jian-Rui ADDITANM: Mang, Jian-Rui		APPLICANT: Drmanac, Radoje T. TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and TITLE OF INVENTION: Polypeptides	FILE REFERENCE: 799 CURRENT APPLICATION NUMBER: US/09/728,952 CURRENT FILING DATE: 2000-11-30	SOFTWARE: DL FL genes Version 2.0 SEO ID NO 40 LENGTH: 1526	TYPE: DNA GRANISM: Homo sapiens	FEATURE: NAME/KEY: CDS TOCHARDN: JEON (1015)	

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68 C-GGGGGGTCTACCTCATGGCCTGTGAGCGTGGACCATTACCCAGCTGTGGTCTGTGC 126
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APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20040014169Alel G Protein-Coupled Receptors
FILE REPERENCE: 00100US1
CURRENT FILING DATE: 2003-08-01
FRICK APPLICATION NUMBER: 60/187, 288
FRICK APPLICATION NUMBER: 60/187, 715
FRICK APPLICATION NUMBER: 60/187, 715
FRICK APPLICATION NUMBER: 60/187, 929
FRICK FILING DATE: 2000-03-08
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                                                                                                      405 CCACTGGGGCCCGCGCTCCGCACGGCTGGCCGCCCAGGCTGGTCTGCGTGGCCATCTG
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Best Local Similarity 98.8%; Pred. No. 1.8e-99;
Matches 403; Conservative 0; Mismatches 1
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US-09-801-944B-64/c
; Sequence 64, Application US/09601944B
; Publication No. US20040014169A1
; GENERAL INFORMATION:
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APPLICANT: Kaytes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Huff, Valerie
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20030003451Alel G Protein-Coupled Receptors Cross-Referen
FILL OF PREPRENCE: 00325, US1
CURRENT APPLICATION NUMBER: US/09/791,932
          1440 CATCCACCCATACAGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCT 1499
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PRIOR FILING DATE: 2000-02-23
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Parodi, Luis A.
Hiebsch, Ronald R.
Lind, Peter
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; ORGANISM: Homo sapiens
US-09-791-932-35
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US-09-791-932-35
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ORGANISM: Homo sapiens
US-10-251-385-77
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                                                                   GIGGTCTGCTTCAGCCCCTACCACCTCAACATCAAGCAGTTCATGGCGAGAGGTATGCTC 437
                                                                                                                                                    CACCTGCCATCCTGTGCCGAGGCGTTTCTTACTGTCCCTTCAGGCCACGGTGGCC 377
                                                                                                                                                                                                    936
                                                                                                                                                                                                                            CTCATGAACATGAACTGTGGCATTACCCC-ATCATTACTTCTTTGCATCCACCATTAC 318
                                                                                                                                                                                                                                                                                   937 AGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                       260 TCCTCCACCCCAGGAAAAGCTTCTTCAGAAACACCCAAGTATCACCCAGGCCAGAGGTTCT 201
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                                                                                                                      CACCTGCCATCCTGTGCCGAGGGGTTTCTTACTGTCCCTTCAGGCCACCGTGGCC 876
                                                                                                                                                                                                                                                                                                                    317 AGGAAATGGCTCCTGGGCATTTTAAAGCTCAAAGGGTCT---TCCTCCTCCTCCTCCTCC 261
556 AGCAGGAAAGGACGCCACTGGCGAGGCTGCTGCTTACGCTGCTGATGCTGGTGGCGGTG 497
                                                                                                                                                                                                  CICATGAACATGAACTGTGGCATTACCCCAATCATTTACTTCTTTGCATCCACCATTAC
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16.7%; Score 184.8; DB 14; Length 1086;
Best Local Similarity 50.6%; Pred. No. 4.8e-43;
Matches 475; Conservative 0; Mismatches 457; Indels 6;
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; Publication No. US20030104487A1
; Publication No. US20030104487A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (GB)
; APPLICANT: Pfizer Inc. (EP except GB, US, JP)
; TILE OF INVENTION: Neuropeptide receptor and uses thereof
; FILE REFERENCE: PCS22032
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: GB 0119920.7
; PRIOR FILING DATE: 2001-08-15
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEO ID NOS: 8
; NUMBER OF SEO ID NOS: 8
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LENGTH: 1086
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TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human (TITLE OF INVENTION: Protein-Coupled TITLE OF INVENTION: Protein-Coupled TITLE OF INVENTION: Protein-Coupled TITLE OF INVENTION: Protein-Coupled TITLE OF INVENTION: Receptors FILE REFERENCE: AREN-0040 CURRENT APPLICATION WUMBER: US/10/251,385 CURRENT FILING DATE: 2002-09-20 PRIOR APPLICATION NUMBER: US/09/170,496 PRIOR PILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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Pred. No. 5.8e-43;
0; Mismatches 457; Indels
                                                                                                                                                                                   ) NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g292056
US-10-305-720-1279
               PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGRAM
SEQ ID NO 1279
LENGTH: 1643
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.6%;
Matches 475; Conservative
                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
TIER REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
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US-10-251-385-205
), Sequence 205, Application US/10251385
); Publication No. US20030105292A1
); GENERAL INFORMATION:
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sal Similarity 50.5%;
474; Conservative
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ORGANISM: Homo
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Pred. No. 7.1e-43;
0; Mismatches 457; Indels 6;
                                                                                                                                                                                                                            APPLICANT: Shiften, Dove APPLICANT: Shiften, Dove APPLICANT: Shiften, Dove APPLICANT: Raser, Matchew R. TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS FILE REFERENCE: PA-0050 US CURRENT APPLICATION NUMBER: US/10/247,671 CTREENT FILING DATE: 2002-09-18 PRIOR FILING DATE: 2001-09-19 NUMBER OF SEQ ID NOS: 186 SEQ ID NOS: 186 SEQ ID NOS: 186 SEQ ID NOS: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID No. US20030194721A1 057385.565
                                                            995 CCTCCTCCACCCAGGAAAGCTTCTTCAGAAACACCA 1032
                                                                                         1037 rgaagricagccccrcaagaarricacgrcaaaar 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or other
                                                                                                                                                                    Sequence 39, Application US/10247671
Publication No. US20030194721A1
GENERAL INFORMATION:
APPLICANT: Mikita, Thomas
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COTHER INFORMATION: a, t, c,
US-10-247-671-39
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OTHER INFORMATION: Incyte
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ORGANISM: Homo sapiens
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Matches 475; Conserv
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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Darek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRW-0040
CURRENT FILIATO DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/99/170,496
PRIOR APPLICATION NUMBER: US/99/170,496
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 205
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968 AGGCTGAAAGGATTACATGGATGTATCCAAACTTTGAAGAAACTAAATCTTCCCT 1027
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Pred. No. 1.4e-42;
0; Mismatches 458; Indels
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ATAAGAGAAAGGTTATGAGGATGCTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTG 1036
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                                                                                                                                 Length 1638
                                                                                                                                      Score 183.2; DB 14; Length
Pred. No. 1.7e-42;
; Mismatches 458; Indels
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Matches 474;
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LENGTH: 1638
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APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1220-4-4
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 66/257,144
PRIOR APPLICATION NUMBER: 66/257,144
PRIOR APPLICATION NUMBER: 00/257,144
NUMBER OF SEQ ID MOS: 2292
SOFTWARE: Patentin version 3.1
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Sequence 90, Application US/09812102
| Patent No. US2002005517941
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TIPLE OF INVENTION: No. US20020055179A1e1 G-Protein Coupled Receptor Homologs
| TIPLE OF INVENTION: No. US20020055179A1e1 G-Protein Coupled Receptor Homologs
| TIPLE REFERENCE: 5800-41 035800/183478
| CURRENT APPLICATION NUMBER: US/09/812,102
| CURRENT FILING DATE: 1999-07-30
| PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
| PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
| NUMBER OF SEQ ID NOS: 90
| SOFTWARE: Patentin Ver. 2.0
| TENGRAL FOR SEQ ID NOS: 90
| TENGRAL FOR SEQ ID NOS: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10498, Application US/09918995
Publication No. U320030073623A1
GENERAL INFORMATION:
APPLICANT: Hyeaq, Inc.
TITLE OF INVENTION: ROWEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     994 TCCTCCTCCACCCCAGGAAAAGCTTCTTCAGAAACACCA 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1134 GIGAAGICAGCCCCTGAAGAAATICACGIGAAATGACA 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: GPCR-RHODOPSIN US-09-812-102-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                          ; Sequence 29, Application US/10350923B
; Publication No. US2004002084A1
; Publication No. US2004002084A1
; GENERAL INFORMATION:
; APPLICANT: Doteon, Stanton B.
; APPLICANT: Day Xiao Jun
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from activ
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from activ
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from activ
; TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from activ
; TITLE OF INVENTION: 009167-0.0
; TILLE REFERENCE: S03157-0.1
; CURRENT APPLICATION NUMBER: US/ 09/454,280
; PRIOR PILING DATE: 1999-12-03
; PRIOR PILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-06-12
; PRIOR FILING DATE: 1999-12-04
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29
: LENGTH: 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 CTCTGTTCTACACAGCCCTCCTGGTGTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGCC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 FTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGCATCTACCTGGTGCACCTGGCTG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 TCATTGTTCAAAACAGGAAAAAAATCAACTCTACCCCCTCTATTCAACAAATTTGGTGA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 TCCAGCTGGCCTTTCGGCAAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCGAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 TGTGCCCACTGGGGCCCGCGCCTCCGCACGGCTGGCCGCCCAGGCTGGTCTGCGTGGTC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580 CTCATGGTCCTGGTGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTGTCC 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 CICTGCATTACAGCCTCGTCTTCATCATTGGGCTCGTGGGAAACTTACTAGCCTTGGTCG 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 finicidánahachtrithaceaceachtriagacenacaceaahacechacharaceahacea 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 ACATATGCAGGTGTGAACTTTATGACCTGAGTATTGACCGCTTCATTGCTGTGTG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 CACCCTCTACGCTACAACAAGATAAAAGGATTGAACATGCAAAAGGCGTGTGCATATTT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 AICTGGACCTŢGGTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCG 519
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Pred. No. 2.6e-39;
0; Mismatches 458; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.5%;
Matches 474; Gonservative (
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US-10-350-923B-29
                                                                                        RESULT 13
US-10-350-923B-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467 CCTTGGTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGG 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 GTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCTGTGTCTG
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                                                                                                                                                                                                                                                                                                                                                               Query Match 11.2%; Score 123.4; DB 10; Length 548; Best Local Similarity 52.8%; Pred. No. 2.5e-25; Matches 262; Conservative 0; Mismatches 234; Indels 0;
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10498
LENGTH: 548
                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(548)
CTHER INFORMATION: n = A,T,C or G
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inear HTC 20-SEP-2003 culus 2 days neonate thymus thymic cells cDNA, RIKEN ngth enriched library, clone:E430001G12 product:EBV-INDUCED sequence. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) P trapper. culus (house mouse) culus ta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; ta; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Braymol. 303, 19-44 (1999)
2019253 1.1 GI:26104619 TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS JOURNAL MEDLINE TITLE

AK087951 Mus muscu CB499474 ssalkhc01 AL547762 AL547762 BX356015 BX356015

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                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Trabhiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer analysis (RISA) system.-384-format
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db_xref="MAI-2426848"
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Achanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Sasistance we gratefully acknowledge.
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Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)

( (bases 1 to 1496)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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Fax:81-45-503-9216)
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/note="Vector: pBlueScriptIISK+; Library Creator: Matthew
In Rise; Atlantic salmon tissue contributors: Carlo Biagi,
Mitch th and Robert Devlin (DFO, Vancouver, B.C.), Simon
Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery (Crofton,
B.C.), Rachel Roper (University of Victoria)"
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(bases 1 to 631)
GRASP Consortium, Davidson, W.S., Koop, B.F. and
A survey of Salmo salar transcripts from high complexity cDNA libraries
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Beetz-Sargent, Maura Busby, Perer Hunt, Linda McKinnel, BF Koop.
bioinformatics: Gordon D Brown.
Location/Qualifiers
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Centre for Biomedical Research
University of Victoria
PO BOX 3020 STN CSC, Victoria BC, VBW 3NS, Canada
Tel: 250 472 4067
Exar: 250 472 4075
Emall: bkcop@wic.ca
Centre for Biomedical Research, University of Victoria cDNA
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16.4%; Score 180.6; DB 14; Length 631;
Best Local Similarity 56.6%; Pred. No. 2.5e-27;
Matches 355; Conservative 0; Mismatches 269; Indels 3;
                                                                                                                  CB499474 linear E:
ssalkhc013018 kidney Salmo salar cDNA, mRNA sequence.
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/mol_type="mRNA"
/strain="McConnell"
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1 (bases 1 to 1097)

1 (Jases 1 to 1097)

Full-length Cruber, C., Jessee, J. and Polayes, D.

Full-length CDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12882129.
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Librally was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6994.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI017CG03QP1&cluster=6994.r. Contact :
Feng Libral BR 1 : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI017CG03QP1.
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                                                                              281 CCAGCTGGCCTTTCGGCAAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCGACA
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                                                                                                                                                            CCTACGGGGGGTCTACCTCATGGCCTGTGAGCGTGGACCATTACCCAGCTGTGGTCT
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1171 bp mRNA linear EST 05-MAY-2003
SX356015 Homo sapiens FLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSOD1007Y101 5-PRIME, mRNA sequence.
BX356015
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1171)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA, libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                 BX356015.1 GI:30382036
                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="texton.9606"
/clone="CSOD1007Y101"
/tissue type="mACENTA" COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirogen. This sequence belongs to sequence cluster 6994.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seq-cSoDi007ABO10P2&cluster=6994.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllengfh.invirogen.com/ InviroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI007ABO10P2.
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Db 435 TTGACTGGAGAATGCCTTGTGTAGGATAACTGCGCTAGTGTTTTACATCAACA 494 Qy 341 CCTACGGGGGGTCTACCTCATGGCCTGTGAGACCATTACCCAGCTGTGGTCT 400 Db 495 CATATGCAGGTGTAACTTTATGACCTGCTGGTATTGACCGCTTCATTGCTGTGGTGC 554 Qy 401 GTGCCCACTGGGGCCGCCGCAACGAGAGGGTGTGAATATTG 614	461 TCTGGACTTGGTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAGGCGGCGTGTGCTCTGGATTTTGAGACTCTCGAGACGCTCCTCATCAAGCAGGGTGTCTGGATTTTGAGACTCTCGAGACGCTCCTCTCATCAAGCAGGGTGTCTCTCAGGATTACATGAGAGAGA	Db 855 AATCTGGTGTAAACAAAAAGGCTCTCAACACAATTATTGTTGTTGTTGTTC 914 Qy 761 TCTGCTTCAGCCCTACCACATCAACACATCATG 801 Db 915 TCTGTTTCACCCTTACCATGTTGCAATTATTCATTGTTGTTGTTGTTC 914 EBSULT 6 BX417963 BX417		Library was constructed by life Technologies, a division of Library was constructed by life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6994.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=cSODE014CD09QPl&cluster=6994.r. Contact : Feng Liang Email: fr/ Lilang@lifetech.com URL : Feng Email: filang@lifetech.com URL : http://tulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODE014CD09QPl. FRATURES Location/Qualifiers	/clssue type="ruthchrith" /clone_lib="Homo sapiens PLACENTA" /note="Vector: $pCMVSPORT_6$; lst strand cDNA was primed
Db 847 TCTGTTTCACACCTTACCATGTTGCAATATCAACATATGATTAAGAAGCTTCGTTTCT 906 Qy	AL532537 LOCUS DEFINITION AL532537 AL532537 Homo sapiens FETAL LIVER Homo sapiens CDNA clone ACCESSION AL532537 Homo sapiens FETAL LIVER Homo sapiens CDNA clone ACCESSION AL532537.2 GI:31070369 KEYWORDS SOURCE ORGANISM Homo sapiens (human) BLS32537.2 GI:31070369 AL532537.2 G	Centre National de Sequencage Grégéenoscope.cns.fr, Web : www.genoscop as constructed by Life Technologies, a di an. This sequence belongs to sequence clus Divaction about this cluster, see W.genoscope.cns.fr/ W.genoscope.cns.fr/ W.jenoscope.com.on/ Linter.cgi?eeq=CSODWOGEB03QPI&cluster=65 Baail : fliang@lifetech.com URL: 11.18-mgth.invitrogen.com/ InvitroGen Corpo Wrenue Genoscope sequence ID : CSODWOGEB3 1. 979 Ancation/Qualifiers 1. 979 Ancation/Qualifiers 1. 979 Ancation-Grow Corpo Ancat	enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	Duery Match 14.5%; Score 160.2; DB 9; Length 979; Best Local Similarity 51.8%; Pred. No. 5.4e-23; Matches 363; Conservative 0; Mismatches 338; Indels 0; Gaps 101 CTCTGTTCTACACAGCCTCCTGGTCTTCAGTGCCTGGGAAACATCCTTGCCTTTGCCTTTGCTTTGCTTTACAGCTTCATTCA	Db 375 TTTCTGATATACTTTTACCACCGCTTTGCCTACAATAGCCTATGGATGG

normalized

second set of porcine ESTs from a pooled-tissue

Library
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Email: smith@email.marc.usda.gov

with phred v0.020425.c and option. Vector identified

Single pass sequencing. Bases called trimmed with the aid of the trim_alt cross match vo.99329.

Plate: RCG8011 row: N column: 14 Seq primer: TAGAAGGCACAGTCGAGG.

Location/Qualifiers

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Query Match
Best Local S
Matches 316
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Best Local Similarity 51.8%; Pred. No. 5.7e-23;
Matches 363; Conservative 0; Mismatches 338; Indels
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DB 14; Length

Score 159.4; DB 14; Length Pred. No. 7.1e-23; 0; Mismatches 261; Indels

tch al Similarity 54.8%; 316; Conservative

/clone lib=!WARC 3PIG"
/note="Vector: pcDNA3.1; Site 1: EcoR1; Site 2: NotI;
/note="Vector: pcDNA3.1; Site 1: EcoR1; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."

/organism="Sus scrofa"
mol_type="mRNA"
db_xref="taxon:9823"
fissue_type="pooled"
lab_host="DH10B"

160

101 CTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTTGCC

464

340

404

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284

460

224

164

104

44

Sus scrofa (pig) Sus scrofa

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

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ses creridearracaecarecrerranaresecrerissaaberrandeeceterra
                                           161 TIACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCTG
                                                                                   523 icattaticaaaacaggaaaaaaaaicaactctaccectriaiattcaaccaactigga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF359817 636 bp mRNA linear 821090 MARC 3PIG Sus scrofa cDNA 3', mRNA sequence. CF359817 GI:34156919
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700

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AGENICOURT 6543842 NIH_MGC_118 homo sapiens cDNA clone IMAGE:5745818 5', mRNA sequence.
BM549799 GI:18785503 EST.
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Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo
                                                                                                                                                                 706 ggaircigcirigggggaigirrcaíaggaiargracriccaciraraáicaircicarci
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TCTGGATTCTAGTATTTGCTCAGACACTCCCACTCCTCATCAACCTATGTCAAAGCAGG
                                                                                 646 AGGCTGAAAGGATTACATGCATGGAGTATCCAAACTTTGAAGAAGTAATGTTCTTCCT
                                             581 TCATGGTCCTGGTGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTGTCCT
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12769 row: g column: 03
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53.8%; Pred. No. 5.1e-22;
tive 0; Mismatches 275; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      761 TCTGCTTCAGCCCCTACCACCTCAACATCAAGCAGTTCATG 801
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Location/Qualifiers
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Best Local Similarity 53.8
Matches 320; Conservative
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Genoscope - Centre National de Sequencage
BP 191 9106 EVAY cedex - France
BP 191 9106 EVAY cedex - France
BP 191 9106 EVAY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6994.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bh/cluster.cgi-Req=CSDD106DE09QP1&cluster=6994.r. Contact :
Feng Liang Email: filangelifetech.com URL:
Feng Liang Email: filangelifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1060DE09QP1.
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                                                    AL551903 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSOD1060XV18 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enritched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                 AL551903
AL551903.2 GI:31273719
                                                                                                                                                                                Homo sapiens (human)
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λ	101	CTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGCC 160	
qc	190	CTCTGCATTACAGCCTCGTCTTCATTGGGCTCGTGGGAAACTTACTAGTGGGTGG	
<i>\</i> 2	161	TTACCTGTCAAAAGAGAGAAGATCAACTGCACAGGGATCTACCTGGTGCACCTGGTG 220	
q	250	TCATTGTTCAAAAACAGGAAAAAAATCAACTGTACACCCTCTATTCAACAAATTTGGTTA 309	
<i>≿</i> ;	221	TGTCTGACCTGCTGTTCACCGTGGCCTTACCGGGAAGGGTGGTGTTATGTGTGTG	
ą	310	TTTCTGATATACTTTTTACCACCGCTTTGCCTACACGAATAGCCTACTATGCAATGGGCT 369	
~	281 (CCAGCTGGCCTTTCGGCAAGGGGCTCTGCAGGCTGACGCGTTTGTGCTCTACACCGACA 340	
ą	370	TTGACTGGAGAATGCGTTGTGTAGGATAACTGCGCTAGTGTTTTACATCAACA 429	
ž.	341 (CCTACGGGGGGGGTCTACCTCATGGCCTGTGGGGGGGGGG	
q	430 (CATALGCAGGTGTGAACTITATGACCTGCCTGAGTATTGACGGCTTCATTGCTGTGGTGC 489	
≿	401 (GTGCCCACTGGGGCCCGCCCTCCGCACGCTGGCCGCCAGGCTGGTTGGCTGGC	
ą	490	ACCCTCTACGCTACAACAAGATAAAAAGGATTGAACATGCAAAAGGCGTGTGCATATTTG 549	
X	461	TCTGGACCTTGGTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGC 520	
ď	550	rciggairciagiairigcidagacaciccacicitaicaacccialgicaaagcagg 609	
≿	521	TGGTGGGCAAGCTGGCATGGAGTACAGCAGGATGGAGTCAGTC	
ą	610 7	AGGCTGAAAGGATTACATGGAGTATCCAAACTTTGAAGAAACTANATCTCTTCCT 669	
⋩	581	TCATGGTCCTGGTGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGGATCCTGTCCT 640	
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ą	730 (GCTATICICAGAICTGCTGCAAACTCTTCAGAACTGCCAAACAAAAAAA 784	

BY765663 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

Mus musculus (house mouse) Mus musculus BY765663.1 GI:27203835 ORGANISM REFERENCE

Fur and substitutes and the state of the state of the state of the state of the state of the state of the state of the state of the state of state linear EST 17-DEC-2002 BY765663 RIKEN full-length enriched, activated spleen Mus musculus CONA clone F830032E22 3', mRNA sequence.

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Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new Genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 34 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a norredundant CDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our weft sit (http://genome.gsc.riken.go.jp) for further details.
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Tel: 91-45-503-9226
Ramil: Genome-geor.riken.go.jp,
URL:http://genome-geor.riken.go.jp,
URL:http://genome-geor.riken.go.jp,
Vadchi,J., Alzawa,K., Akimura,T., Azakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Noojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,R., Shibata,R., Shiraki,T., Tagami,M.,
Takeda,Y., Watki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw Boris, A., Yanagiawa, M., Yang, Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Arakwa, T., Fukuda, A., Harah, X., Bakai, M., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation Nature, 420, 563-573 (2002)
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/clone_lib="RIKEN full-length enriched, activated spleen"
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14.1%; Score 155.2; DB 13; Length 715;
Best Local Similarity 52.9%; Pred. No. 5.6e-22;
Matches 359; Conservative 0; Mismatches 313; Indels 6; Gaps
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Sandelin. Schneider, C. Sembider, C. S. Sandelin. S. Dischelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. Strandelin. St
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/tissue_type="FETAL LIVER"
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/clone_lib="Home sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCWVSPORT 6 vector. Library was not normalized."
       clone="CS0DM009YF17"
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                                                                   TIACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCTG 220
                                                                                                                                                                                                                                                                                                                                                                                                                          401 GTGCCCACTGGGGCCCGCGCCTCCGCACGGCTGGCCGCCCAGGCTGGTCTGCGTGCCCA 460
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BP 191 91006 EVRY cedex - France
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Brail: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6994.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAM009CC09QP1&cluster=6994.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAM009CC09QP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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FEATURES

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                                                                                                                                    101 CTCTGTTCTACACACCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGCC 160
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MRNA linear EST 18-DEC-we64e01.x1 Soares thymus NHF7H Homo sapiens cDNA clone
IMAGE:2245880 3' Similar to SW:BBI2 HUMAN P32249 EBV-INDUCED G
PROTEIN-COUPLED RECEPTOR 2 ;, mRNA Sequence.
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                                                                     0; Gaps
13.6%; Score 150.6; DB 13; Length 1201; 53.6%; Pred. No. 5.9e-21; Live 2; Mismatches 266; Indels 0;
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                                                                     Matches 309; Conservative
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SM Mus musculus

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;

Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 662)

3 (kazaki Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nixaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Sala, B. Dragani, T.A.,

Chochia, C., Corbani, L.B., Cousins, S., Gaasterland, T.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Kawaji, H., Kawasawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                289 CCTTTCGGCAAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCGACACCTACGGG 348
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                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1014 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 408.
Location/Qualifiers
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471 GGGGTCTACCTCATGGCCTGTGTGAGCGTGGACCATTACCCAGCCGTG 424
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                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2345880"
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Reversely, N. Pellali, R. Ponnisa, T. U. Gip. P. Remachanton, S. Ringwald, M., Sandelin, S. Schneider, C., Sengio, C., Second, S. Shindea, K., Sandelin, S. Schneider, S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. Sandea, R. Shindea, R. S. Shindea, R. S. Shindea, R. S. Shindea, R. Shindea, R. S. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Shindea, R. Sh
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Pred. No. 1.6e-19;
0; Mismatches 222; Indels 0;
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Bases 1 to 861)

S NIH-MGC http://degc.nci.nih.gov/.

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Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: BI768868 861 bp mRNA linear EST 25-SEP-2001 BI768868.1 GI:15760446 Homo sapiens (human) mRNA sequence. BI768868 Homo sapiens VERSION KEYWORDS SOURCE ORGANISM RESULT 15 BI768868 LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION

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ADGWCALHRHLRGWYLMACWSWDHYPAVVCAHWGPRLRTAGRARLWCWAIWTLVLLQ

GADGWCALHRHLRGWYLMACWSWDHYPAVVCAHWGPRLRTAGRARLWCWAIWTLVLLL

TMPLLLMPWTWFLWGYLACMEYSWESVLGAPLMVLWARAIGFGGFWGVILLSCYMKIT

WKLCSTAGRYQTAREDPYTSGKGRHRRDSFGGPSDQDGRTFPLARLPAYAADAGGRGGI

MCDRLPDCHQAWHGERDAPPAILCRAGGELWYSGGHRGPHEHELWHYPFIYFPASTHYR

KWLLGILKLKGSSSSSSSSSSSSSTPGKASSETPSITQARGSMFLAEHV" ή. 156 1020 1080 1080 PAT 04-MAR-2003 900 900 096 960 840 Suwa, M., Amai, K., Akiyama, Y. and Aburatani, H.

Guanosine triphosphate-binding protein coupled receptors

Patent: EP 1270724-A 1293 02-JAN-2003;

National Institute of Advanced Industrial Science and Technology

(JP); Center for Advanced Science and Technology Incubation, Ltd.

(JP) 780 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. CGCTCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTT TCAGAAACACCAAAGTATCACCCAGAGGTTCTATGTTCTTAGCGGAGCACGTGGTC 841 AGGCTTTCTTACTGTCCCTTCAGGCCACCGTGGCCCTCATGAACATGAACTGTGGCATT AAGCTCAAAGGGTCTTCCTCCTCCTCCTCCTCCTCCTCCACCCCCAGGAAAAGCTTCT CTCAACATCAAGCAGTTCATGGCGAGAGGGATGCTCCACCTGCCATCCTGTGCCGAGCGG AGGGCTTTCTTACTGCCCTTCAGGCCACCGTGGCCCTCATGAACATGAACTGTGGCATT ACCCCAATCATTTACTTCTTTGCATCCACCCATTACAGGAAATGGCTCCTGGGCATTTTA ï Length 4319; 41.8%; Score 461; DB 6; Length 43 clarity 99.8%; Pred. No. 3.5e-258; Conservative 0; Mismatches 0; Indels linear /mol_type="unassigned DNA" /db_xref="taxon:9666" join[010...308,3128...3531,3660...4119) /note="unnamed protein product" /codon_start=1 DNA 4319 bp D1 Sequence 1293 from Patent EP1270724. AX647101.1 GI:28800143

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TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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Direct Submission

Direct Submission

Direct Submission

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

on Apr 12, 2001 this sequence version replaced gi:13276997.

During sequence assembly date is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                            CGCTCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTT
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MPORTANT: This sequence is not the entire insert of clone RP11-178C10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-178C10 is at 98861 in this sequence. The true right end of clone RP11-461N23 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6215. .6548 ...
horte="Charliel repeat: matches 2292. .2629 of consensus" 6557. ...
6635 / note="L2 repeat: matches 2128. .2206 of consensus" 6730. .7233 ...
horte="L2 repeat: matches 1330. .1889 of consensus" 8301. .8499 / note="MIR repeat: matches 17. .219 of consensus"
SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Purther information can be found at http://www.sanger.ac.uk/RGDP/Chri3 RP11-178C10 is from the library RPCI-11.1 constructed by the group of Pieter de Jong Por further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACG3.6
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13491. .14076
/note="Li repeat: matches 2226. .2881 of consensus"
(6310. .17185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11.1"
161. .463
/note="liMB8 repeat: matches 5836. .6160 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              656 .723
/noce="12 repeat: matches 2592. .2659 of consensus"
2385. .2420
/note="MMK repeat: matches 111. .146 of consensus"
4555. .4446
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.23981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1855. .4646
'note="12 repeat: matches 1031. .1120 of consensus"
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note="L2 repeat: matches 1551. .1656 of consensus"
079. .9126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2708 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1554. .9754
note="MER20 repeat: matches 33. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1989. .5306 -
note="MER7A repeat: matches 2. .345 of consensus"
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note="FAM repeat: matches 2. .165 of consensus"
0402. .10703
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/note="24_copies 2 mer at 75% conserved"
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'note="LIM1 repeat: matches 5264.
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'note="L2 repeat: matches 2574.
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1. .98861
/organism="Homo sapiens"
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/clone="RP11-178C10"
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2510 /not 2574 /not /not /not /not	Consensu 26005 /nocess 26209 /note="A /note="A /note="T /note="T /note="T		41119. 41175. 41175. 41175. 41483. 41483. 41791.	/3250. 4927/9 /note="15 copies 2 mer ca 100% conserved" 44262. 44708 /note="MLT1C repeat: matches 1466 of consensus" 4486045178 /note="MLT2FB repeat: matches 1328 of consensus" 452445235 /note="16 copies 2 mer tg 87% conserved" 4538945539 /note="MRESB repeat: matches 4175 of consensus" 456394578 repeat: matches 9184 of consensus" 4563946788 /note="MRESA repeat: matches 25250 of consensus" 4628146837 /note="MRERTD repeat: matches 1510 of consensus" 4784618877 repeat: matches 1510 of consensus" 478461884618837	/ 700 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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56802 GCTGTGTCTGACCTGCTGTTCACCGTGGCCTTACCGGGAAGGGTGGTGTGTTATGTGCTG 56743
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// note="Willing repeat: matches 437. .541 of consensus" 57462. .57560 // note="Willing repeat: matches 169. .264 of consensus" 57462. .57560 // s0462 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0464 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0463 // s0
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Best Local Similarity 99.8%; Pred. No. 4.1e-258;
Matches 581; Conservative 0; Mismatches 0; Indels 1.
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AC016189 151174 bp DNA linear HTG 13-JUL-2000 Homo sapiens clone RP11-23M9, LOW-PASS SEQUENCE SAMPLING. AC016189

LOCUS DEFINITION ACCESSION

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     Sirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Callymare, A., Cangelo, M., Collymare, A., Cooke, P., DeArellano, K., Damar, K., Collymare, A., Cooke, P., PitzHugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Howland, J.C., Johnson, R., Grant, G., Kann, L., Karatas, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Horton, L., McEwan, P., McGwan, K., McLaughlin, J., Meldrim, J., McGwan, P., McGwan, P., McGwan, C., Marchand, P., Marquis, N., Stange-Thomanni, N., Stoffanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasalliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Myman, D., Ye, W.J., Zimmer, A. and Zody, M. Olly I. Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA Charles Helpi, Mwww.seq.wi.mit.edu Center for Genome Research Center code: WIER Web site: http://www-seq.wi.mit.edu Contact: sequence submissions@genome.wi.mit.edu Center project name: 23_M_99
                                                                                Eukaryogin, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I Chases I to 151174)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-23M9
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
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             AC016189.3 GI:9129134
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                               HTG; HTGS_PHASE0.
Homo sapiens (human)
                                                                    Homo sapiens
                                                                                                                                                                            Unpublished
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139048 TGCATGGAGTACAGCATGAGTCAGTCATCGGCTCCCTCATGGTCCTGGTGGCC 139107
  Homo sapiens clone RP11-23M9, LOW-PASS SEQUENCE SAMPLING.
AC016189: 3 GI:9129134
HTG: HTGS PHASE0.
Homo sapiens (human)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                  CIGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGGGCAAGCTGGCC
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15.9%; Score 176; DB 6; Length 536;
Best Local Similarity 99.6%; Pred. No. 6.3e-91;
Matches 226; Conservative 0; Mismatches 1; Indels
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Patent: WO 0162797-A 35 30-AUG-2001;
PHARWACIA & UPJOHN COMPANY (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 35 from Patent WO0162797.
AX230148
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Best Local Similarity 99.8
Matches 488; Conservative
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8: contrig of 934 bp in length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-23M9
Unpublished
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 CTCATGAACATGAACTGTGGCATTACCCCA 347
                                                                              Vogeli, G. and Wood, L.S.
G protein-coupled receptors
Patent: WO 0166750-A 64 13-SEP-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers

    .556
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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      Homo sapiens
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47488: contig of 846 bp in length 48488: gap of 100 bp 48488: gap of 100 bp 48548: gap of 100 bp 48548: gap of 100 bp 50383: contig of 902 bp in length 48550: contig of 802 bp in length 50383: contig of 802 bp in length 51453: gap of 100 bp 51352: contig of 846 bp in length 52406: gap of 100 bp 51352: contig of 848 bp in length 52424: gap of 100 bp 51352: contig of 834 bp in length 52424: gap of 100 bp 51352: contig of 834 bp in length 52424: gap of 100 bp 51352: contig of 834 bp in length 51452: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 5185: gap of 100 bp p in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 845 bp in length 61885: contig of 849 bp in length 61885: contig of 849 bp in length 61885: contig of 849 bp in length 61885: contig of 849 bp in length 61885: contig of 849 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 61850: gap of 100 bp 6180 bp in length 6180: gap of 100 bp 6180 bp in length 6180: gap of 100 bp 6180 bp in length 6180: ga
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Sequence 64 from Patent WO0166750.
AX244735
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Birren, B. (Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campoplano, A., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, A., Cook, B., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Cand-Pierre, N., Gardyna, S., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Michar, C., Macdonald, P., Major, J., Marquis, L., Norban, C., Nicol, R., Mihova, T., Mlenga, V., Murphy, T., Nay, Dr., J., Way, Dr., V., Way, Dr., V., Pollara, V., Raywond, C., Retta, R., Phukhang, P., Pierre, N., Pollara, V., Raywond, C., Retta, R., Phukhang, P., Pierre, N., Pollara, V., Santos, R., Santos, R., Schupback, R., Stange-Thomann, N., Schupback, R., Stange-Thomann, N., Subramanian, A., Tavats, N., Tesfaye, S., Theodore, J., Topham, K., Travers, N., Travers, N., Travers, N., Travers, N., Travers, N., Travers, N., Travers, N., Travers, N., Viel, R., W, W., Viel, R., Wilson, B., Wilson, D., Ye, W, J., Young, G., Viel, R., Vol, N., Yillson, B., Wilson, D., Ye, Waman, D., Ye, W., J., Young, G.,
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Mus musculus chromosome 10, clone RP23-46412, complete sequence.
AC117702
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Medentia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 14755)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 10, clone RP23-46412
Unpublished
2 (bases 1 to 147559)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 CACCTGCCATCCTGTGCCGAGGGGGTTTTTTACTGATCCCTTCAGGCCACGTGGCC 377
                                                                                                                                                                                   697 AGCAGGAAAGGACGCCACTGGCGAGGCTGCCTTACGCTGCTGATGCTGGTGGCCGTG
                                                                                                                                                                                                                                    757 GIGGICIGCIICAGCCCCIACCACCICAACAICAGCAGIICAIGGCGAGAGGGAIGCIC
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                                                                                                 Gaps
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         DB 6; Length 556;
tch
al Similarity 99.5%; Pred. No. 6e-81;
209; Conservative 0; Mismatches 1; Indels
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AX244735.1 GI:15859614 Homo sapiens (human) clone="RP23-464I2" clone_lib="RPCI-23 Female Mouse BAC"

repeat_region repeat_region

us-10-041-615-33.oli10.rge

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Direct Submission

Direct Submission

Submitted (307-NOV-2033) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 14755)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,

Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,

Boguelavkiy,L., Boukhalter,B., Camarata,J., Cahang,J., Choepel,Y.,

Collymore,A., Cook,A. Cook,P., Cortis,L., Erickson,J., Faro,S.,

Rereira,P., Fitzderald,M., Gagel,D., Galdgan,J., Gardyna,S.,

Rant,A., Karatas,A., Kells,C., Landers,T., Levine,R.,

Indblad-Toh,K., Liu,X., Lui,X., Mabbitt,R., MacLean,C.,

Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,

Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,

Nguyen,C., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,

Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,

Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,

Spencer,B., Stange-Thomann,V.S., Viel,R., VohA., Wilson,B.,

Vassiliev,H., Venkataraman,V.S., Viel,R., VohA., Wilson,B.,

Nabmitted (44-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker:html
                                                               Direct submission

Submitted (10-ARR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE Birren, 320 Charles Street, Cambridge, MA 02141, USA

CE Birren, B. Nusbaum, C. Lander, E., Abouelleil, A., Allen, N., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H. W., Corwis, J., Chang, J., Choepel, Y., Collymore, A., Cook, P., Corwis, E., Erickson, J., Faro, S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Grahami, L., Grand-Plerre, N., Hafez, N., Galagan, J., Gardon, P., FitzGerald, M., Gage, D., Galagan, D., Hagopian, D., Hagopian, D., Hadon, K., Hall, J., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Liud, G., Lui, X., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Mahowa, T., Mangay, V., Murphy, T., Naylor, J., Norbu, C., Nachen, S., Severt, P., Peters, N., Newlin, J., Schupes, R., Peter, R., Ries, C., Rogov, P., Roman, J., Schauer, S., Schupesck, P., Senan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submistra, Control Manda, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Submitted, Worker, Submistra, Control Manda, D., Wallson, M., Wallson, B., Manda, M., Milson, B., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Manda, M., Mand
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Center: Whitehead Institute/ MIT Center for Genome Research
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------- Project Information
Center project name: 1.24127
Center clone name: 464_1.2
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
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Only the last 147.6 kilobases of this clone are being submitted. The remainder overlaps accession number AC113207 [WICGR project L23741].

Location/Qualifiers
1. 147559
/organism="Mus musculus"
/mol_type="genomic DNA"

FEATURES

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/rpt_family="(GA)n"
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/note="single clone coverage"
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Rattus norvegicus clone CH230-6015, WORKING DRAFT SEQUENCE, 4
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94177 AGGGTCTTCCTCCTCCTCCTCCTCCTCCTCC 94144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.1%; Score 34; DB 10; L
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                                  .21383
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Act venome sequencing consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24941437.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends off the clone and there may be sequence may extend beyond the ends off the clone and there may be sequence shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O. Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Parternak, S., Paul, H., Perez, A., Perez, L., Prantenak, C., Plopper, F., Polndexcer, A., Perez, D., Pranten, D., L. L., Plopper, F., Polndexcer, A., Popovic, D., Pranten, E., Du, L. L., Phazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigly, R., Reilly, M., Relly, M., Ren, Y., Regier, M.A., Reigly, R., Railly, B., Reilly, M., Ren, Y., Rose, M., Rose, M., Raiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Slsson, Y., Sitter, C.D., Smajs, D., Shetty, J., Sodergren, E., Song, X.-Z., Sotelle, R., Soas, J., Shen, H., Strong, R., Sutton, A., Syatek, A., Tabor, P., Taylor, T., Thomas, N., Thomas, D., Waldern, B., Walden, J., Walker, B., Wang, J., Walge, D., Wallson, R., Wallson, D., Walder, B., Wooden, H., Wozley, R., Walczyk, R., Woden, H., Wozley, K., White, F., Waight, D., Wright, R., Wilson, R., Walzer, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R., Smith, D.R., Holt, R.A., Smith, H.O., Niederlausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission

AL Upublished

S. Morley, K.C.

Direct Submission

AL Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

S. Rat Genome Sequencing Consortium.

Real Direct Submission

By Plaza, Houston, TX 77030, USA

Real Genome Sequencing Consortium.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 237786 bases at least Q30
Consensus quality: 239195 bases at least Q20
Estimated insert 248197; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Center project name: GGAQ
Center clone name: CH230-6015
Assembly program: Atlas;
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The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kivchii, S., Satch,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Obneda,E., Yahagi,W., Suzuki,K., Li,C., Confsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakmai,K., Kurosaki,T., Kodama,T., Mauda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Kawamata,M., Yoshimura,A., Mixura,J., Kawamata,M., Yoshimura,A., Mixura,J., Kawai,J., Carninci,P., Adachi,J., Alaxawa,K., Riffeli,K., Sakawi,J., Carninci,P., Adachi,J., Alaxawa,K., Ishii,Y., Itch,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osako,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Voshino,M., and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                 AK067772 1695 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J013120L23, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK067772.1 GI:32977790

FI_CDNA, CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enrhartoideae; Oryzeae; Oryza.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
                                                                                                     Length 227;
                                                                                                     Query Match
3.0%; Score 33; DB 8; Lv
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                    973 TCTTCCTCCTCCTCCTCCTCCTCCTCCACC 1005
                                                                                                                                                                                                                                                  98 TCTTCCTCCTCCTCCTCCTCCTCCTCCTCCACC 130
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Science 301 (5631), 376-379 (2003)
/rpt_type=tandem
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AK067772/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tao,N., Barbaruk,W.B., Liu,J., Wu,K. and Barry,G.F.
Direct Submission
Submitted (10-3NA-2001) Genomics, Monsanto, 800 North Lindbergh
Blvd., Crove Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
Location/Qualifiers
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1. (base) 1 to 227)

Tao, M., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
Simple sequence repeats from Monsanto rice genomic sequences
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Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 34; Conservative 0; Mismatches 0; Indels
6 237355: gap of unknown length
6 238603: contig of 1148 bp in length
4 238603: gap of unknown length
4 239798: contig of 1195 bp in length
9 239898: gap of unknown length
9 242813: contig of 2915 bp in length.
Location/Qualifiers
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COMMENT

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FIRMGLPIIGGLSSEPTNVKKAAGIDYDSFVATTIALGTRVKETKRLLDGSKGKEDGC
LTKLRSFPESAEBELKVITBEQLRIMELVKKTTNYYQAGALKERNLFQLFVIIRDFLG
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Boweer, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., J., Jones, T., Kamiya, R., Narin-Neumann, G., Kawai, J., Lim, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A. Direct Submission and Ecker, J.R.
Direct Submission Salk Institute Genomic Analysis Laboratory (StGnAn), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; RIKEN stabidopsis Full-Length cDNA); Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Bowser, L., Chan, M.M., Chang, C.M., Male, J.M., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.
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/note="This clone is in pUNI 51"
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/codon_start=1
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/protein_id="Ang62880.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%; Score 33; DB 8; Length 2790;
llarity 100.0%; Pred. No. 6.1e-07;
Conservative 0; Mismatches 0; Indels
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       Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 105-8602, Japan (E-mail: skikuchledias, affrc.go.jp, Tel: 81-29-88-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashiran, Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yanada, H., Ooka, H., Hotta, T., Kojima, K., Namiki, T., Innikawa, M., Yanada, H., Ooka, H., Hotta, T., Kojima, K., Naikiki, T. and Yamamoto, M. Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Kurosaki, T., Kurosaki, T., Kurosaki, T., Kurosaki, T., Kurosaki, T., Kurosaki, T., Kurosaki, T., Kurosaki, T., Kurosaki, Y., Tsunoda, Y., Uu, M., Nasuka, M., Narikawa, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Uu, M., Nav, M., Kae, O., Yokomizo, S., Yoshimura, A., Matsubara, K. and Mrakami, K., Narikawa, K., Harangaki, T., Arawawa, T., Carninci, P., Pukuda, S., Hanagaki, T., Harangawa, T., Aramagawa, T., Ranagawa, T., Ranagawa, T., Ranagawa, T., Ranagawa, T., Matsuyama, K., Nomo, H., Kawai, T., Koda, M., Kawai, T., Koda, M., Kawai, T., Koda, S., Kurihara, C., Matsuyama, T., Matsuyama, T., Matsuyama, K., Nomura, K., Numasaki, R., Ohno, M., Obato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, C., Yagawa, A., Taya, M., Matsuyami, F., Yasunishi, P., Saitoh, H., Sakai, C., Sakai, K., Yagawa, A., Tayan, M., Tayan, H., Tanka, T., Tanaka, T., Tayan, Y., Tayan, A., Tayan, F., Yasunishi, F., Yasunishi, R., Tand, H., Tanaka, T., Tanaka, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T., Tayan, T.,
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Bowser, L., Carninci, P.,
Dale, J.M., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Rarlin, Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Cnodera, C.S., Palm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,
Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A.
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domain-containingprotein (At1g59910) mRNA, complete cds.
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/cultivar="Nipponbare"
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/clone="J013120L23"
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Query Match

ORIGIN

FEATURES

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RESULT 12

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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

ACCESSION VERSION KEYWORDS

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Gaps

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                 100332 SP159 bp DNA linear HTG 22-NOV-2001
s musculus clone RP23-126G16, LOW-PASS SEQUENCE SAMPLING.
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                        Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (Dases 1 to 59159)
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows

overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

will be sequenced to completion. In the event that

* the record is updated, the accession number will

be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center: sequence Information
Center project name: L15119
Center clone name: 126_G_16
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Direct Submission

Direct Submission

Direct Submission

Submitted (14-FBB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Boukhgalter, B., Camarata, J., Chospel, Y., Collymore, A., Cook, A., Cook, P., Corum, B.) DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, I., Erickeon, J., Faro, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Hafez, N., Hagopian, D., Hagos, S., Hall, J., Horton, L., Hulme, W., Hafez, N., Matthews, C., McCarthy, M., Madchan, L., Manchen, C., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Major, J., Mahone, J., Major, J., Manning, J., Matthews, C., McCarthy, M., Najor, J., Major, J., Schauer, S., Schupback, R., Seman, S., Schubs, M., Stojanovic, N., Stubbs, M., Stona, J., Tesfaye, S., Theodore, J., Tophan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, V., Stojanovic, N., Stubbs, M., Vassiliev, H., Vonkataraman, V.S., Viel, R., Tavers, M., Vassiliev, H., Vonkataraman, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, V.S., Viel, R., Zainoun, R., Saver, C., Spencer, Submission

Research, 320 Charles Street, Cambridge, MA 02141 USA

All repeats were identified using RepeatMasker: html

Rutt, A.F.A., & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                    Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Ander, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cook, P., Corrum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, F., Dorrie, L., Erickson, J., Faro, S., Farreira, P., Firsderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Indolad-Toch, K., Liu, G., Liu, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Minor, T., Mlenga, V., Murphy, T., Naylor, J., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Senan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Klubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Mannan, D., Young, G., Zainoun, J., Limmer, A., and Zody, M. Direct Submission.
                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 78244)
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                       Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 8, clone RP23-439N24
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Center clone name: 439_N_24
HTG; HTGS PHASEO.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 78244)
   KEYWORDS
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Mus musculus chromosome 8 clone RP23-439N24 map 8, LOW-PASS
SEQUENCE SAMPLING.
AC140499.2 GI:31075328
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Matches 33;
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DEFINITION ACCESSION VERSION

RESULT 14 AC140499

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and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                   gap of 100 bp in length contig of 934 bp in length gan of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap of 100 bp in length gap
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APU04394 (japonica cultivar-group) chromosome 2 clone OLYZA SAFORES COSTILE CO6, *** SEQUENCING IN PROGRESS ***.
APU04394. GI:17402600
HTG; HTGS PHASE2.
OLYZA SATIVA (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryzea; Oryza. ö 3.0%; Score 33; DB 2; Length 78244; 100.0%; Pred. No. 7.3e-07; ive 0; Mismatches 0; Indels 1: gap of 100 bp 7: contrig of 966 bp in length 7: gap of 100 bp 8: contrig of 940 bp in length 8: gap of 100 bp 8: contrig of 938 bp in length 8: contrig of 938 bp in length 9: gap of 100 bp 9: gap of 100 bp 7: contrig of 935 bp in length 9: gap of 100 bp 7: contrig of 935 bp in length 9: gap of 100 bp 7: contrig of 939 bp in length 9: gap of 100 bp 7: contrig of 945 bp in length 9: gap of 100 bp 9: contrig of 945 bp in length 9: gap of 100 bp 9: contrig of 945 bp in length 9: gap of 100 bp 9: contrig of 949 bp in length 9: gap of 100 bp 9: contrig of 949 bp in length 9: contrig of 949 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 940 bp in length 9: contrig of 941 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 942 bp in length 9: contrig of 943 bp in length 9: gap of 100 bp 9: contrig of 943 bp in length 9: gap of 100 bp 9: contrig of 943 bp in length 9: gap of 100 bp 9: contrig of 945 bp in length 9: gap of 100 bp 9: contrig of 945 bp in length 9: gap of 100 bp 9: contrig of 945 bp in length 9: gap of 100 bp 9: contrig of 945 bp in length 9: gap of 100 bp 74932 TCTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC 74964 973 TCTTCCTCCTCCTCCTCCTCCTCCTCCACC 1005 47415: 47515: 48555: 49498: 49598: 54711: 54811: 55753: 55853: 56764: 334957. 3350957. 3360957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 340957. 7819: 58849: 11547: 6864: :0627: 647: 587: 7919: 3.0 Best Local Similarity 100. Matches 33; Conservative 333892 3349938 3359938 3359998 3369998 33700998 33700998 3391020 3391020 3391020 3491039 4410158 44101 52688 53661 53761 54712 55751 55854 56765 RESULT 15 AP004394 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION g ઠ

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REFERENCE

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Outpulshed Only in Database (2001)

AL Published Only in Database (2001)

RS Sasaki,T., Matsumoto,T. and Yamamoto,K.

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Aprobiological Science, Rice Genome Research Program; Kannondai Agrobiological Science, Rice Genome Research Program; Kannondai (B-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469

Tel:81-298-38-7441, Fax:81-298-38-7469

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-dapan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the combining Monsanto and RGP-dapan sequence of the gaps between the are represented as runs of N. The order of the gaps between the are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence.

* NoTE: This is a soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers

* Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"

/organism="Opponent DNA"

/oultivar="Nipponent"

/db_xref="taxon:39947"

/chromosome="2"

/clone="0J1118_C06"
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OJ1118 C06
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Matches 33; Conservative 0; Mismatches 0;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

February 21, 2004, 19:27:14; Search time 483 Seconds (without alignments) 9710.167 Million cell updates/sec Run on:

US-10-041-615-33 1104 1 atgataaaactaggccctta......gtgtcatttgctttatgact 1104 Title: Perfect score: Sequence:

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3373863 seqs, 2124099041 residues Searched:

10 Word size : 1958023 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

M_Geneseq_29Jan04:*

1: geneseq11980s:*

2: geneseq11990s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	CDNA e		7 Human	Aas98131 Human DNA	N	_	9 DNA en	Human	Human	-	9 Human	. Probe	7 Human	Aai47743 Probe #16	Human	Probe	Aak41698 Human bon	Aak15953 Human bra	Human	Aai08137 Probe #81		Aai13216 Probe #31	Aba54915 Human foe	
ID	ABS64723	ADC86840	AAK76477	AAS98131	ABK94922	AAS98111	AAS78869	AAS42840	AAS30791	AAS98061	ABA15489	AA122451	ABA67527	AA147743	ABA49623	ABA34608	AAK41698	AAK15953	ABS41287	AA108137	ABS15705	AAI13216	ABA54915	
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Aai34569 Probe #32	2 Human	Aba24683 Probe #31	Aak28643 Human bon	0	Human	Aai03121 Probe #31	N	Aaa92174 Oryzias l	Aaa92175 Oryzias l	Medaka	Aaz46519 Murine CA	4 Human	9 Human	Aai50733 Probe #19	Aak44756 Human bon	Human	Abs44416 Human liv	Abs18995 Human gen	C	Probe	Aba70492 Human foe	
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guanosine triphosphate-binding protein coupled receptor; gene therapy
                                                                                                      AAGCTGTGCAGCACAGCTCGGGAGGACCCAGTGACCAGGAAAGGACGCCACTGGCGA
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                                                                   ATGGAGTACAGCATGCATGGAGTCAGTCCTCGGGCTGCCCCTCATGGTCCTGGTGGCCTTTT
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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P-PSDB; ADC86841.
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                                                                                 This invertion relates to a may isolated deprotein coupled receiptor to polypeptide, GPCRX mucleic acid and an antibody specific to the protein care useful for treating, preventing or alleviating a GPCRX associated disorder to pathological state in a subject, particularly a human. In particular, the disorder is cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing and metabolic pathway or modulation. The GPCRX polypeptide and nucleic acid are also useful for diagnosing the presence of or predisposition to a disease associated with alterapeutic or prophylactic applications for disorders associated with alterapeutic or prophylactic applications for disorders associated with abermant GPCRX expression or activity, e.g. von Hippel-Lindau syndrome, the abermant GPCRX expression or activity, e.g. von Hippel-Lindau syndrome, abermant GPCRX expression activity, e.g. von Hippel-Lindau syndrome, abermant GPCRX expression, and isease, cerebral palsy, epilepsy, lescho-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, contractions disease, untuington's disease, infertility, asthman syndrome, multiple sclerosis, ataxia-telangiectasia, contractions, or graft-versus -host disease, infertility, human immunity asthma, arthritis, human contraction, scleroporosis, inflammatory bowel disease, infertility, hypertension, scleroderma, haemophilia, asthma, arthritis, human contraction, susful in gene therapy for treating the above conditions. The protypeptides can be useful in developing powerful associated chromosome mapping, tissue typing, preventive medicine, and chromosome mapping, tissue typing, preventive medicine, and as indiagnostic applicational analysis of various human disorders, as well as invantion and human of protein coupled receptor related protein GPCRN of the invantion
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                                                                   This invention relates to a new isolated G-protein coupled receptor (GPCRX) polypeptide sequence and the CDNA encoding it. The GPCRX
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100.0%; Score 1104;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1104; Conservative 0; Mismatches
   Claim 9; Page 97; 252pp; English
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
              cytostatic; gene therapy; vaccine; metastasis; ds
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08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
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                                                               WO200157182-A2
                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516
                                                                                       The invention relates to a novel polynucleotide encoding a guanosine triphosphare-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphare-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     336
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           New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                               TGCCTTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTG
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                                                              Claim 1; SEQ ID NO 1293; 28pp; English
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Matches 581; Conservative
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25- SEP-2000; 2000US-023493PF.
27- SEP-2000; 2000US-0234844P.
29- SEP-2000; 2000US-0235836P.
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29- SEP-2000; 2000US-0235836P.
20-0CT-2000; 2000US-0235836P.
20-0CT-2000; 2000US-0235893P.
20-0CT-2000; 2000US-023937P.
20-0CT-2000; 2000US-023937P.
20-0CT-2000; 2000US-024647P.
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20-0CT-2000; 2000US-024920P.
20-0CT-2000; 2000US-024920P.
20-0CT-2000; 2000US-024920P.
20-0CT-2000; 2000US-
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

controlled and polymucleotides may be used in the prevention, diagnosis and
treatment of diseages associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
controlled the activity of mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)

controlled may be used to produce the secreted (I), by inserting the
controlled may be used to produce the secreted (I), by inserting the
controlled into a host cell and culturing the cell to express the
controlled and treat immune/haematopoletic-related diseases, especially
concers and cancer metastesses of haematopoletic-derived cells. AAK64703

concers and cancer metastesses of haematopoletic-derived cells. AAK64703

concers and cancer metastesses of haematopoletic antigen genomic
concers and cancer metastesses of haematopoletic antigen genomic
concers from the present invention. AAK54942 to AAK84950 and AAM92169 GCCATCTGGACCTTGGTGCTGCTGCAGACGATGCCCTTGATGATGATGACCAAG 516 493 GCTGTGTCTGACCTGCTGTCACCGTGGCCTTACCGGGAAGGGTGGTGTGTTATGTGCTG 552 GACACCTACGGGGGGGTCTACCTCATGGCCTGTGAGCGTGGACCATTACCCAGCTGTG 396 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. CCCCTCATGGTCCTGGTGGCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTG 97 CGCTCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTT 157 TGCCTTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTG 373 GGCTCTCTGTTCTACACAGCCCTCCTGGTGTTCAGTGCCCTGGGAAAACATCCTTGCCCTT 217 GCTGTGTCTGACCTGCTGTTCACCGTGGCTTTACCGGGAAGGGTGGTGTTATGTGCTG 0; Indels 1; Gaps Disclosure; SEQ ID NO 31289; 3071pp + Sequence Listing; English. Sequence 9409 BP; 2123 A; 2163 C; 2259 G; 2864 T; 0 U; 0 Other; Query Match
Best Local Similarity 99.8%; Pred. No. 9.4e-217;
Matches 581; Conservative 0; Mismatches 0; Indels Ruben SM; 05-JAN-2001; 2001US-0259678P. (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC, WPI; 2001-483426/52. 337 397 672 457 732 517 792 577 셤 ठे 8 8 8 Š Š ઠ ò 셤 ઠે

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disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the invention
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                                                                                                                                                                                                                                   1001 TCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCTTTGC
                                                                                                                                                                                                                                                                               160 CTTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCT
                                                                                                                                                                                                                                                                                                                                                                         881 GIGITCIGACCIGITCACCGIGGCCTIAACCGGGAAGGGTGGTGTTATGTGTGCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGCCCACTGGGGCCCGCGCTCCGCACGGCTGGCCGCCCAGGCTGGTCTGCGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGCCCACTGGGGCCCGCGCCTCCGCACGGCTGGCCGCCCAGGCTGGTCTGCGTGGCC
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                                                                                                                                                                                                                  TCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTTGC
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                                                                                                                                                Length 1001;
                                                                                                               Sequence 1001 BP; 190 A; 315 C; 311 G; 185 T; 0 U; 0 Other;
                                                                                                                                                Score 458; DB 6; Length 10
Pred. No. 2.8e-215;
0; Mismatches 0; Indels
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                                                                                                                                                41.5%;
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                                                                                                                                            Query Match
Best Local Similarity 99.8
Matches 578; Conservative
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Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing.
                                                                                                                                               Claim 1; Page 403-404; 672pp; English.
                                           30-NOV-2001; 2001WO-US047004.
                                                      30-NOV-2000; 2000US-00728952.
                                                                                                  WPI; 2002-508509/54.
P-PSDB; ABG66698.
                                                                                Tang YT, Goodrich
Yamazaki V, Ujwal
                                                                    (HYSE-) HYSEQ INC.
                  WO200244340-A2
       Homo sapiens.
                               06-JUN-2002
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The invention relates to human novel polymucleotides and associated polypeptides. The polymucleotides and polypeptides are useful for treating inflammatory conditions such as arthitis, nebritis, Crohn's disease, ischiammatory conditions such as arthitis, inepritials, Crohn's disease, ischiammatory conditions such as attenties, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemoteactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, cartilage, treadment injament and/or nerve tissue growth tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritiap, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia directions, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABK944800-ABK94981 represent human converses the novel polymucleotides of the invention

Ouery Match 37.0%; Score 409; DB 6; Length 1526; Best Local Similarity 99.7%; Pred. No. 4.1e-191; Matches 579; Conservative 0; Mismatches 1; Indels 1 Sequence 1526 BP; 282 A; 458 C; 458 G; 328 T; 0 U; 0 Other;

157 217 ACACCTACGGGGGGGCTACCTCATGGCCTGTGAGCGTGGACCATACCCAGGTGGG 397 481 541 277 crererereacerecreteredecerraceseaacererererarereredes 601 GCTCCAGCTGGCCTTTCGGCAAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCG 337 GCTCCAGCTGGCCTTTCGGCAAGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACG GCTCTCTGTTCTACACAGCCCTCCTGGTCTTCAGTGCCCTGGGAAACATCCTTGCCCTTT GCTCTCTGTTCTACACACACCCCCCGGGTCTTCAGTGCCCCTGGGAAACATCCTTGCCCTTT GCCTTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGG GCCTTACCTGTCAAAAGAGCAGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGG CTGTGTCTGACCTGCTGTTCACCGTGGCCTTACCGGGAAGGGTGGTGTTATGTGCTGG Gaps ۲; 98 422 158 482 218 542 278 602 338 ద à 셤 ò d 셤 ò à ઠે

780 517 840 577 900 637 960 457 CCCTCATGGTCCTGGTGCCTTTGCCATTGGCTTCTGTGGCCCAGTGGGGATCATCCTGT 662 ACACCTAC-GGGGGGTCTACCTCATGGCCTGTGAGCGTGGACCATTACCCAGCTGTGG TCTGTGCCCACTGGGGCCCGTGCCTCCGCACGGCTGGCCGCGCCAGGCTGGTCTGCGTGG CCCTCATGGTCCTGGTGGCCTTTGCCCATTGGCTTCTGTGGGGCCAGTGGGGGATCATCCTGT TCTGTGCCCACTGGGCCCCGCCCTCCGCACGCTGGCCCGCCAGGCTGGTCTGCGTGG 961 cerecrarardadearcaceredadecrerecadeacacaci 1001 678 CCTGCTATATGAAGATCACCTGGAAGCTGTGCAGCACAGCT 398 721 458 518 578 901 638 g à В g d ò à 8 ઠે

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Wang

Wang J,

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Asundi

Zhou P, RT;

Liu C, 2 Drmanac F

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RESULT 6

BP. AAS98111 standard; DNA; 330

AAS98111;

12-MAR-2002 (first entry)

Human DNA for potential G protein-coupled receptor #68.

Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atcherosclerosis; basal carcinoma; breast carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; carcinoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; oscenoarthritis; osteoporosis; parkinson's disease; psoriasis; rheumatorid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; osteoprish; diabetes; phyperlipidaemia; stroke; gene therapy.

Homo sapiens.

WO200185791-A1.

15-NOV-2001.

11-MAY-2001; 2001WO-US015332.

11-MAY-2000; 2000US-0203217P. 18-MAY-2000; 2000US-0205945P.

(LIFE-) LIFESPAN BIOSCIENCES INC.

WPI; 2002-066595/09.

Brown JP, Miller M,

Pritchard D;

Burmer G, Fabre-Suver C,

Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis, stroke

Claim 2; Page 83; 144pp; English.

The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host

Mon Feb 43 11:38:46

cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, represence, agonists or antagonists of the novel GPCR polypeptides including the GAL4 polypeptide. The antibodies and mucleic acid probes as carefulding the GAL4 polypeptide. The antibodies and mucleic acid probes of an nucleic acids and are used to diagnose a variety of diseases or disorders in which GPCRs are involved e.g., Allzeimer's disease, anyotrophic lateral sclerosis, athma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic constructive pulmonary disease, Crobia diseases, depression, epilepsy, macular degeneration, lymphoma, melanoma, multiple sclerosis, costeoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid archititis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, pain perception classes disorders, cardiovascular activity disorders, pain perception clasorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polymoration.

Sequence 330 BP; 46 A; 101 C; 108 G; 75 T; 0 U; 0 Other;

TGGGGCCCGCGCCTCCGCACGCCTGGCCCAGGCTGGTCTGCGTGGCCATCTGGACC 468 528 180 240 AAGCTGGCCTGCATGGAGTACAGCAGCATGGAGTCAGTCCTCGGGCTGCCCCTCATGGTC 588 1 GGGGTCTACCTCATGGCCTGTGTGAGCGTGGACCATTACCCAGCTGTGGTCTGTGCCCCAC 60 TTGSTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGGTGCC 349 GGGGTCTACCTCATGGCCTGTGAGCGTGGACCATTACCCAGCTGTGGTCTGTGCCCAC TTGGTGCTGCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGGGC 0; Gaps Ouery Match 28.8%; Score 318; DB 6; Length 330; Best Local Similarity 100.0%; Pred. No. 3.1e-146; Matches 318; Conservative 0; Mismatches 0; Indels AAGATCACCTGGAAGCTG 666 AAGATCACCTGGAAGCTG 318 409 469 121 529 181 649 301 g g 셤 셤 ð g ઠે 원 ઠ ò ò

DNA encoding novel human diagnostic protein #14673 AAS78869 standard; cDNA; 1771 BP (first entry) 13-FEB-2002 AAS78869; Human;

1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder;

Homo sapiens.

WO200175067-A2

11-OCT-2001

us-10-041-615-33.01110.rng

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73 P-PSDB; ABG14682 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 14673; 103pp; English.

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymucleotides are also used and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cappend to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. AAS4197-AAS9564 represent novel human diagnostic coding sequences of the involved. The sequence data for this patent did not appear in the printed specification, but was obtained in partners and the printed specification, but was obtained in the contract of the involved of the contract of the contr electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1771 BP; 313 A; 531 C; 519 G; 407 T; 0 U; 1 Other;

Gaps 7 Length 1771; Query Match
25.3%; Score 279; DB 5; Length 17
Best Local Similarity 99.4%; Pred. No. 5.4e-127;
Matches 499; Conservative 0; Mismatches 2; Indels

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982 graccirccecacederecedecedeceaecresicreceredecearcresacerresiderecr 536 357 476 297 861 416 981 801 921 802 ACCGIGGCCTTACCGGGAAGGGTGGTGTTATGTGCTGGCTCCAGCTGCCTTTCGGC 298 AAGGGGCTCTGCAGGCTGACGGCGTTTGTGCTCTACACCGACACCCTACGGGGGGGTCTAC 922 CTC%IGGCCTGIGIGAGCGIGGACCAITACCCAACTIGIGGICIGIGCCCACTGGGGCCC 742 AGGAAGATCAACTGCACAGGCATCTACCTGGTGCACCTGGCTGTGTCTGACCTGCTGTTTT 862 AAGGGGCTCTGCAGGGCTGACGGCGTTTGTGCTCTACACGGGACACCTACGGGGGGGTCTAC 238 ACCGIGGCCTIACCGGGAAGGGIGGIGITAIGIGCIGGGCTCCAGCIGGCCTTTCGGC 358 CTCATGGCCTGTGTGAGCGTGGACCATTACCCAGC-TGTGGTCTGTGCCCACTGGGGCCC 417 GCGCCTCCGCACGGCTGGCCGCCCAGGCTGGTCTGCGTGGCCATCTGGACCTTGGTGCT 477 GCTGCAGACGATGCCCTTGCTCTTGATGCCCATGACCAAGCCGCTGGTGGGCAAGCTGGC 엄 à g ઠ 셤 ઠે 셤 à 셤

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WO200166750-A2.
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             Human, G-protein coupled receptor; GPCR; mental disorder; schizophrenia; attention deficit disorder; anxiety; depression; bipolar disorder; ss; metvological disorder; Huntington's disease; dementia, Dobsity, anorexia; metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis; type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer; cardiomyopathy; atherosclerosis; human imminodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser; antidepressant; anorectic; PCR primer; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for cDNA molecules encoding human G-protein coupled receptor (GPCR) polypeptides. The protein and DNA sequences of the invention can be used to identify compounds which bind to GPCR polypeptides and in screening
                                       CITTGCCATTGGCTTCTGTGGGCACGTGGGATCATCCTGTCCTGCTATATGAAGATCAC
 CTGCATGGAGTACAGCATGGAGTCAGTCCTCGGGCTGCCCCTCATGGTCCTGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity.
                                                                                                                                                                                                                        Human G Protein-Coupled Receptor (GPCR) cDNA #35.
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                                                                                              CTGGAAGCTGTGCAGCACAGCT 1243
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                                                                                  CTGGAAGCTGTGCAGCACAGCT 678
                                                                                                                                                          AAS42840 standard; cDNA; 536 BP.
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23-FEB-2000; 2000US-0184303F.
23-FEB-2000; 2000US-0184304P.
23-FEB-2000; 2000US-0184305P.
23-FEB-2000; 2000US-0184397P.
03-MAR-2000; 2000US-0186457P.
09-MAR-2000; 2000US-0188064P.
13-MAR-2000; 2000US-0188064P.
23-UNN-2000; 2000US-0188806.P.
23-UNN-2000; 2000US-0213861P.
11-JUL-2000; 2000US-0213861P.
11-JUL-2000; 2000US-021337P.
14-JUL-2000; 2000US-0218337P.
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for compounds that modulate GPCR activity. By screening a human subject theor the presence of mutations in GPCR DNA, a GPCRErelated disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, demental and bipolar disorder, neurological disorders such as Huntington's disease, Parkinson's disease and Tourette's syndrome, metabolic disorders such as thrombosis, moreatia and type 2 diabbetes, cardiovascular disorders such as thrombosis, myocardial infarction, cardiovascular disorders such as viral infections caused by HIV and cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 176; DB 4; Length 53
Pred. No. 3.4e-76;
0; Mismatches 1; Indels
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2000US-0187582P.
2000US-0187714P.
2000US-0187715P.
2000US-0187828P.
2000US-0187829P.
2000US-0187839P.
2000US-0187839P.
2000US-0187834P.
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AAS30791/c
ID AAS30791 standard; CDNA; 556
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Best Local Similarity 99.6
Matches 226; Conservative
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The invention relates to novel isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x. nGPCR-x polymucleotides, c polypeptides, and modulators may be used in the treatment of diseases and conditions such as infections, such as viral infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, antherosclerosis), Parkinson's disease, and psychotic and neurological atherosclerosis), Parkinson's disease, and psychotic and neurological atherosclerosis), Parkinson's disease, and psychotic and neurological atherosclerosis), Parkinson's disease, and dyskinsesis, such as Huntington's disease or Tourette's Syndorme and many other diseases and syndormes in listed in the specification. nGPCR-x polynucleotides and polypeptides, as used as nGPCR-x modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence encodes a G protein-
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                                                                                                                                                         Isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and schizophrenia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 GIGGICHGCHICAGCCCCTACCACCTCAAGCAGTTCAIGGCGAGAGGATATGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coh 14.4%; Score 159; DB 4; Length 55 al Similarity 99.5%; Pred. No. 8.2e-68; 209; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                          Claim 4; Page 204-205; 336pp; English.
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                                                                 (PHAA ) PHARMACIA & UPJOHN CO
08-MAR-2000; 2000US-0187929P.
08-MAR-2000; 2000US-0187930P.
08-MAR-2000; 2000US-0188049P.
08-MAR-2000; 2000US-0189294P.
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Best Local Similarity
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                                                                                           Vogeli G,
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Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; carcinoma; carcinoma; carcinoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma;

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The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequence (including antiennse probes), a host cell comprising an expression vector comprising the GPCR sequence.

CC antibodies raised against the polypeptides are useful for identifying modulators of the polypeptides are useful for identifying modulator compounds which function as modulators, activators, impussors, agonists or antagonists of the novel GPCR polypeptides or including the GAL4 polypeptide. The antibodies and mucleic acid probes as including the GAL4 polypeptide. The antibodies and mucleic acid probes or including the GAL4 polypeptide. The antibodies and mucleic acid probes and mucleic acids and are used to disgnose a variety of disease.

CC described above can be used to disgnose a variety of diseases or disorders in which GPCRs are involved e.g., Alzheimer's disease or disorders in which GPCRs are involved e.g., Alzheimer's disease.

CC arcinoma, breast carcinoma, asthma, atherosclerosis, basal cell carcinoma, presence of the polypeptides are also obstructive pulmonary disease, Ccolm's disease, depression, epilepsy, constending the specification. The probes and antibodies are also useful for disapporosis, Parkinson's disease, parorasis, hormonal crelease disorders, andrewish, hormonal crelease disorders, andrewish, hormonal crelease disorders, andrewish, hormonal crelease disorders, andrewish, hormonal crelease disorders, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can disorders, be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene continued.
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multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia; ulcerative colitis; tuberculosis, cognition disorder; memory disorder; ancrexia, hormonal release disorder, cardiovascular activity disorder; pain perception disorder; obesity, diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy.
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llarity 100.0%; Pred. No. 3.4e-40;
Conservative 0; Mismatches 0;
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18-MAY-2000; 2000US-0205945P.
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    Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HyV; antibacterial; vulnerary; antiparkinsonian; autisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antishergic; antidiabetic; antiuloer; antionulsant; antifungal; antiparasitic; cardiant; immune discorder; cardiovascular discret; neurological disease; infection; nephrotropic; gene therapy; vaccine; de.
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                                                                              ABA15489 standard; DNA; 22760 BP
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2000US-0231244P

2000US-0231414P

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2000US-023238P

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17-NOV-2000;
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Homo sapiens.

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring in a expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fication, but was ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%; Score 31; DB 4; Length 232; 100.0%; Pred. No. 0.00011; tive 0; Mismatches 0; Indels
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03-AUG-2000) 2000US-0053366.
21-SEP-2000) 2000US-02368FP.
24-SEP-2000) 2000US-023559P.
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26-MAY-2000; 2000US-0207456F.
30-UUN-2000; 2000US-00608408.
33-AUG-2000; 2000US-00632366.
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Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenical; (b) immune considers e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, theumatoid arthritis and ulcerative collisis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases such as wiral, bacterial, fungal and parasatici infections. Note: The sequence data for this patent did not form part of trom WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #12384 for gene expression analysis in human cervical cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 7820; 1701pp + Sequence Listing; English.
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                                                          17-NOV-2000; 2000US-024929F.
17-NOV-2000; 2000US-024930DP.
10-DEC-2000; 2000US-025193PP.
05-DEC-2000; 2000US-025198PP.
05-DEC-2000; 2000US-025198PP.
05-DEC-2000; 2000US-0251856P.
06-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
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RESULT 12 AAI2245:

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Claim 25; SEQ ID NO 16429; 654pp; English

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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                                                                                                                                               nucleic acid probes useful for analyzing
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100.0%; Pred. No. 0.00011;
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gene expression in human fetal liver.
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26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-023468FP.
27-SEP-2000; 2000US-023468FP.
04-OCT-2000; 2000GB-00024263.
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                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                      Hanzel DK, Chen W,
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-CCT-2000; 2000GB-00024263.
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                                                                                                                   WPI; 2001-483447/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful
                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                                                                 Sequence 232 BP; 12 A; 94 C; 5 G; 119 T; 0 U; 2 Other;
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235589.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
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Best Local S:
Matches 31
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information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 88888888

Sequence 232 BP; 12 A; 94 C; 5 G; 119 T; 0 U; 2 Other;

Query Match 2.8%; Score 31; DB 4; Length 232; Best Local Similarity 100.0%; Pred. No. 0.00011; Matches 31; Conservative 0; Mismatches 0; Indels

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Search completed: February 21, 2004, 21:44:41 Job time : 487 secs g

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February 21, 2004, 21:28:30; Search time 109 Seconds (without alignments) 5620.787 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                           US-10-041-615-33
1104
1 atgataaaactaggccctta......gtgtcatttgctttatgact 1104
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Sequence 4, 7
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/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
/cgn2_6/ptodata/2/ina/6A_COMB.seg:*
/cgn2_6/ptodata/2/ina/6B_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-371-489-4
US-09-571-849-12
US-09-517-849-13
US-09-517-849-13
US-09-517-849-13
US-09-517-849-13
US-09-517-849-13
US-09-517-849-13
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US-08-680-038-16
US-08-68-747-4
US-08-68-747-4
US-08-68-747-4
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US-08-580-923-34
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                                                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length D
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                              Run on:
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No.
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15, Appl 15, Appl 37, Appl 37, Appl 37, Appl 54, Appl 1, Appl		M	Gaps	
Sequence Seq		1F-SUBUNII GENE	114; s 0;	GENE
US-08-860-038-15 US-09-580-923-15 US-09-517-849-37 US-09-517-849-37 US-09-187-330-4 US-09-187-330-4 US-09-187-330-1 US-09-620-3120-619 US-09-620-3120-619 US-09-620-3120-619 US-09-620-3120-619 US-09-265-617B-1 US-09-265-617B-1 US-09-135-241-1 US-09-807-166-1	ALIGNMENTS	RESULT 1 US-09-495-714C-5/C Sequence 5, Application US/09495714C Sequence 5, Application US/09495714C GENERAL INFORMATION: TITLE OF INVENTION: RETINAL CALCIUM CHANNEL TITLE OF INVENTION: RETINAL CALCIUM CHANNEL TITLE OF INVENTION: RETINAL CALCIUM CHANNEL UNRENT APPLICATION NUMBER: US/09/495,714C CURRENT FILING DATE: 2000-02-01 NUMBER: OF SEQ ID NOS: 138 SOFTWARE: PatentIn version 3.1 SEQ ID NO 5 LENGTH: 6114 TYPE: DNA TYPE: DNA COGANISM: MUS musculus US-09-495-714C-5	imilarity 100.0%; Pred. No. 2.2e-05; Conservative 0; Mismatches 0; Indel TCTTCCTCCTCCTCCTCCTCCTCCTCCT 1003	US/08899595 Shuh L. No. 6111072uaki RHO TRGET PROTEIN HUMAN MDIA AND 14 SS: E Lardner reet, N.W., Suite 500 W: NY disk compatible PC-DOS/MS-DOS PR-BCASS #1.0, Version #1.30 ANA:
558 558 558 558 558 558 558 558		nn US/09 nn US/09 rechno terinal 3.4 (for TOMBER: 7000-0 138 srsion 3	2.8%; 100.0%; ative rccrccrc	on US/088 hai, Shuh hith Oo. EECODI SESS: EI EECODI Street, N OCEM: OCEM: COMPATA:
4444444444444444		C-5/c Application 6670465 ORMATION: University T NVENTION: RET ENCE: 45499.4 PLICATION NUM LING DATE: 2 SEQ ID NOS: 1 Patentin vers 114 Mus musculus C-5	Similarity 100.0%; P 1; Conservative 0; TCTTCCTCCTCCTCCTCCTCTTCTTCTTCTTCTTCTTCT	Sequence 4, Application US/08899595 Sequence 4, Application US/08899595 Barent No. 6111072 APPLICANT: Narumiya, Shuh APPLICANT: TARABBAIN No. 61110 TITLE OF INVENTION: RHO TARGET TITLE OF INVENTION: RHO TARGET TITLE OF INVENTION: ENCODING SA NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardher STREET: 3000 K Street, N.W., CITY: Washington COUNTRY: USA COUNTRY: USA ZIP: 2007-5109 COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: Patentin Release #1 CURSPERMENT APPLICATION DATA:
000000000000000000000000000000000000000		LT 1 9.495-714C-F guence 5, Ag tent No. 66 NERAL INFORM NETLE OF INVI ITLE OF INVI UMBER OF SER OF TREE OF TRE	Query Match Best Local Sir Matches 31; Y 973 TV	ESULT 2 Sequence 4, Applicati Batent No. 6111079: GENERAL INFORMATION: APPLICANT: Marumi APPLICANT: Takaha TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD STREET: 3000 K CITY: Washingto STREET: D.C. COUNTRY: USA ZIP: 2000 TSA ZIP: 2000 TSA CONFUTER READABLE MEDIUM TYPE: COMPUTER: IBM FOOMETIER COMPUTER: IBM FOOMETIER SOFTWARTING SYSTEM SOFTWARTING SYSTEM CORRENT APPLICATION
2226666666666444444 80001264666680012642		ULT 1 09-499 equent atent atent APPLIC TITLE FILE 1 CURRED CURRED NUMBEI SOFTW EQ 1D LENG TYPE ORGAN	uery est I	RESULT 2 Sequent Seque
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) NAME/KEY: misc_feature
; LOCATION: (223)
; OTHER INFORMATION: VANCO B PMP-PROBE 496.20 (ON PMP) IN EXAMPLE 16
US-09-371-489-4
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2.6%; Score 29; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Anand Natrajan
APPLICANT: Qingping Jiang
APPLICANT: Qingping Jiang
APPLICANT: David Sharpe
APPLICANT: Bay-Jong Law
TITLE OF INVENTION: NEAR INFRARED CHEMILUMINESCENT
TITLE OF INVENTION: ACRIDINITUM COMPOUNDS AND USES THER
TITLE OF INVENTION: CCDLT-2588X
CURRENT APPLICATION NUMBER: US/09/371,489
CURRENT APPLICATION NUMBER: 60/096,073
EARLIER APPLICATION NUMBER: 60/096,073
EARLIER PILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
SEQ ID NO 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Le
6.7e-05;
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2.7%; Score 30; DB
Best Local Similarity 100.0%; Pred. No. 6.7
Matches 30; Conservative 0; Mismatches
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     Sequence 4, Application US/09371489 Patent No. 6355803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-979-608A-12/c
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US-08-899-595-5/C

US-08-899-595-5/C

Sequence 5, Application US/08899595

Patent No. 6111072

Patent No. 6111072

APPLICANT: Narumiya, Shuh

APPLICANT: Takahashi, NO. 6111072

TITLE OF INVENTION: ENCODING SAME

TITLE OF INVENTION: ENCODING SAME

TITLE OF INVENTION: ENCODING SAME

TITLE OF INVENTION: ENCODING SAME

TITLE OF INVENTION: ENCODING SAME

TORRESPENDENCES: 14

CORRESPONDENCES: ADDRESS:
ADDRESSEE: FOLEY & Lardner

STARE: D.C.

COUNTY: USABILISTON

MEDIUM TYPE: FOLEY disk

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk

COMPUTER: LEM PC Compatible

COMPUTER: LEM PC Compatible

CORRENT APPLICATION NUMBER: US/08/899,595

FILING DATE: 24-JUL-1997

CLASSIFICATION NUMBER: UP 8-242701

PILING DATE: 24-JUL-1997

CLASSIFICATION NUMBER: UP 8-242701

PILING DATE: 24-JUL-1997

APPLICATION NUMBER: UP 9-90170

FILING DATE: 25-MER-1997

APPLICATION NUMBER: UP 9-9170

FILING DATE: 25-MER-1997

APPLICATION NUMBER: UP 9-9170

FILING DATE: 25-MER-1997

APPLICATION NUMBER: UP 8-10170

FILING DATE: 25-MER-1997

APPLICATION NUMBER: UP 8-10170

FILING DATE: 25-MER-1997

APPLICATION NUMBER: UP 8-10170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%; Score 30; DB 3; Length 5822; Best Local Similarity 100.0%; Pred. No. 6.7e-05; Matches 30; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/899,595
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION NUMBER: UP 9-90170
PILING DATE: 26-AUG-1996
PRIOR APPLICATION NUMBER: UP 9-90170
PILING DATE: 25-ARR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent REGISTRATION NUMBER: 04941/0112
REFERENCE/DOCKET NUMBER: 04941/0112
TELEERAX: (202)672-5399
TELEERAX: (202)672-5399
TELEERAX: (202)672-5399
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MOLECULE TYPE: CDNA tO MENA
ORIGINAL SOURCE:
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28..3972
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; LOCATION:
US-08-899-595-4
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FARENT NO. 05.252.3.

FARENT LOES, AND M.
APPLICANT: Lees, AND M.
APPLICANT: Lees, AND M.
APPLICANT: Lees, AND W.
APPLICANT: Lees, Sumon W.
APPLICANT: Lees, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPRENCE: 10.97-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PLILING DATE: 1997-11-26
PRIOR PLILING DATE: 1997-11-26
PRIOR PLILING DATE: 1997-10-27
PRIOR PLILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
2.6%; Score 29; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0; Indels
                                        MEDIUM TYPE: IBM Compatible
COMBUTER: IBM Compatible
SOFTWARE: RestERG for Windows Version 2.0
SOFTWARE: RestERG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: A2-MAY-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: A2-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REFERENCE/DOCKET NUMBER: 10797-003001
TELEFRATION UNDER: 35,965
TELEFRATION INFORMATION:
TELEFRANCE (17/542-806
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1362 base pairs
TYPE: NUCLEIC acid
STRANDENESS: single
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SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-517-849-12
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Patent No. 6632923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   972 GICTICCICCICCIC
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; LOCATION: (1)...(696)
US-09-616-289-12
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Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Louis
REGIGTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION:
TELEPHONE: 617/542-5070
TELEFRAX: 617/542-8906
INFORMATION FOR SEQ ID NO. 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 29; DB 4; Length 1362;
100.0%; Pred. No. 0.0002;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTENCE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
ATTORNEY/AGENT INFORMATION:
                                                                         TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        972 GICTICCICCICCICCICCICCICCICCI 1000
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STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                            ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arjona, Anibal A. TITLE OF INVENTION: NOVEL LOW DENSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCATION: 1...696 SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-08-979-608A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence
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Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1362 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                STATE: MA
COUNTRY: USA
ZIP: 02110-284
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                  NUMBER OF SEQUENCES: 42
                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100."
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
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US-09-517-849-12/C
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; Patent No. 6605588
; GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: BER Compatible

COMPUTER: BER Compatible

CORPUTER: BER Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FRESENG for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/979,608A

FILING DATE: 26-No. 6355451-1997

PRILING DATE: 03-JUN-1997

PRILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REFERENCE/DOCKET NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 35,965

TELECOMMUNICATION NUMBER: 10797-002001 (formerly 3983/59818)

TELECOMMUNICATION NUMBER: 15,965

REFERENCE/DOCKET NUMBER: 15,965

REFERENCE/DOCKET NUMBER: 15,965

REFERENCE/DOCKET NUMBER: 15,965

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2.6%; Score 29; DB 4; Length 1422;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0; Indels
                                                              Query Match
2.6%; Score 29; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Tchardson P.C.
STREET: 225 Franklin Street
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US-08-979-608A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-979-608A-13/c; Sequence 13, Application US/08979608A; Patent No. 6355451; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-517-849-13/c
; Sequence 13, Application US/09517849
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lees, Ann M.
Lees, Robert S.
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                          NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Simon M.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ARD THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
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                                                                                                                                                                              Query Match
2.6%; Score 29; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         972 GICTICCICCICCICCICCICCICCI 1000
                                                                               NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
SITREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1...756
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coding Sequence
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09616289
Patent No. 6632923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1422 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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Gaps
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                                      Score 29; DB 4; Length 1617;
Pred. No. 0.0002;
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                                                                              .0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RELIAGION NUMBER: US/09/517,849
FILING DATE: 02-MAT-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 4;
Pred. No. 0.0002;
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                           2.6%; bcc.
100.0%; Pred. No. c.
... 0; Mismatches
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100.0%; Pred. No. vo...
0; Mismatches
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US-09-517-849-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richards
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                        Sequence 11, Application US/09517849
Patent No. 660558
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09616289 Patent No. 6632923
                                                                                                                                                                                                                                                                                                                                                                             Arjona, Anibal A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                  972 GICTICCICCICCICCI
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Best Local Similarity 100.
Matches 29; Conservative
                                                                            29; Conservative
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                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                    RESULT 12
US-09-517-849-11/c
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US-08-979-608A-11
                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                         Length 1422;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
Lees, Ann M.
Lees, Robert S.
Law, Simon M.
Azjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
COMPATION SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NO. 6355451-1997
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING PROTEINS AND THE TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                    Score 29; DB 4;
Pred. No. 0.0002;
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FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
    PRIOR FILING DATE: 1997-11-26
PRIOR PELICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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PRIOR APPLICATION NUMBER: US 08/979,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08979608A
Patent No. 6355451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
                                                                                                                                                                                                                                                                                                                                    Query Match
2.6%; Soc
Best Local Similarity 100.0%; P:
Matches 29; Conservative 0;
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Oryctolagus cuniculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: (1)...(756)
US-09-616-289-13
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US-08-111-939-1
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GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lew S. Simon M.

APPLICANT: Law, Simon M.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-27

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 48

LENGTH: 2561

TYPE: DATE

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APPLICANT: Law, Jamon W.
APPLICANT: Law, Jamon W.
APPLICANT: Arjona, Annbal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 10797-004001
CURRENT PAPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/79,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER: OF SEQ 1D NOS: S3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ DN O1 11
LENGTH: 1617
TYPE: DNA
CREATION: COPYCTOLAGGUS CUNICULUS
CREATION: COPYCTOLAGGUS CUNICULUS
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Patent No. 6632923
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; LOCATION: (246)...(1895)
US-09-616-289-48
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; LOCATION: (1)...(951)
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Query Match Best Local Similarity

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GENERAL INFORMATION:
APPLICANT: Rawai, Shinji
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Amani, Bgon
TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
TITLE OF INVENTION: Protein and Process for its Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3728;
                                                                                                          Query Match
2.6%; Score 29; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
Sequence 1, Application US/08111939
Patent No. 5460951
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MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: double
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Search completed: February 21, 2004, 23:47:00 Job time : 115 secs

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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published Applications NA:* 1: /cm2 6/ptodata/2/mihpna/HS07 PUBCOMB.seg:*	2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*	ဖြ	4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*	z	_6/ptodata/2/pubpna/PCTU	6/ptodata/2/pubpna/US08	6/ptodata/2/pubpna/US08	ω	!	1 1	6/ptodata/2/pubpna/US09	 _6/ptodata/2/	<pre>15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*</pre>	_6/ptodata/2/pubpna/US10	/pubbna/US60	<pre>18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*</pre>	
Database																	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 33, Appl	Sequence 1619, Ap	Sequence 1293, Ap	Sequence 40, Appl	Sequence 35, Appl	Sequence 64, Appl	Sequence 90, Appl	Sequence 19928, A	Sequence 3149, Ap	Sequence 5532, Ap	Sequence 1941, Ap	Sequence 1, Appli	Sequence 27614, A	Sequence 17166, A	Sequence 22442, A
US-10-041-615-33	US-10-017-161-1619	US-10-292-798-1293	US-09-728-952-40	US-09-791-932-35	US-09-801-944B-64	US-09-812-102-90	US-09-864-761-19928	US-09-864-761-3149	US-10-260-238-5532	US-10-260-238-1941	US-09-893-666A-1	US-09-864-761-27614	US-10-029-386-17166	US-09-864-761-22442
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Sequence 17651, A Sequence 1021, Ap Sequence 1031, Ap Sequence 10977, A Sequence 871, App Sequence 5679, App	Sequence 6520, Ap Sequence 30250, A Sequence 3466, Ap Sequence 273400, Sequence 20317, A		22224	Sequence 450, App Sequence 411, App Sequence 411, App Sequence 497, App Sequence 497, App Sequence 496, App Sequence 496, App Sequence 496, App Sequence 1377, App
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ALIGNMENTS

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and	1104;	0
ULT 1 10-041-615-33 equence 33, Application US/10041615 ubilcation No. U520040014038A1 EMERAL INFORMATION: APPLICANT: Casman, Staten APPLICANT: Ellerman, Karen APPLICANT: Ellerman, Karen APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Elderman, Karen APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Son USSO10-10-10-3 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 CURREN APPLICATION NUMBER: 60/260,544 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,77,405 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,544 PRIOR FILING DATE: 2001-01-09 CURRENT APPLICATION NUMBER: 60/20,544 PRIOR FILING DATE: 2001-01-09 APPLICATION: 400-09 CURRENT APPLICATION NUMBER: 60/20,544 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATION: 400-09 APPLICATI	Length 1104;	Indels
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SULT 1 -10-041-615-33 -110-041-615-33 SQUEGNEC 33, Application US/10041615 Publication No. US20040014038A1 GENERAL INFORMATION: APPLICANT: Casman, Stacie J APPLICANT: Edinger, Shlomit R APPLICANT: Edinger, Shlomit R APPLICANT: Edinger, Shlomit R APPLICANT: Edinger, Shlomit R APPLICANT: Edinger, Salonit R APPLICANT: Padigaru, Muralidhara APPLICANT: Padigaru, Muralidhara APPLICANT: Padigaru, Muralidhara APPLICANT: Padigaru, Muralidhara APPLICANT: Padigaru, Muralidhara APPLICANT: Padigaru, Muralidhara FILE REFERENCE: 21402-233-061 CURRENT PILING DATE: 2001-01-09 PRIOR APPLICATION NUMBER: 60/260,544 PRIOR APPLICATION NUMBER: 60/277,405 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-01 SOOTWARE: CURSCELLIST Version 0.1 LENGTH: 1104 TYPE: DNA CRGANISM: Homo sapiens FRATURE: NAME/KST: COS ILOCATION: (1)(1080)		Larity 100 Conservative
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RESULT 1 US-10-041-615-33 Feducace 33, Applico Publication No. US2, GENERAL INFORMATION APPLICANT: Caeman, APPLICANT: Caeman, APPLICANT: Ellarm APPLICANT: Ellarm APPLICANT: Endinge APPLICANT: Endinge APPLICANT: Padiga TITLE OF INVENTION FILE REFERENCE: 21, CURRENT APPLICATION FILE REPERENCE: 21, CURRENT APPLICATION FRIOR FILING DATE: PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR FILING DATE:	tch.	Best Local Similarity Matches 1104; Conserv
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3060 GCTGTGTCTGACCTGCTGTTCACCGTGGCCTTACCGGGAAGGGTGGTGTTATGTGCTG 3119
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US-10-17-161-1619

Sequence 1619, Application US/10017161

Sequence 1619, Application US/10017161

Sequence 1619, Application US/10017161

Sequence 1619, Application US/10017161

APPLICANT: SUWA, MAKIKO

APPLICANT: SUWA, MAKIKO

APPLICANT: ASAT, KIYOSAII

APPLICANT: ASAT, KIYOSAII

APPLICANT: ASATYAMA, YUTAKA,

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR APPLICATION NUMBER: JP 2001/246789

SEQUENCE: SEQUENCE: 2.10

SEQUENCE: SEGUENCE: 2.11

SEQUENCE: SEGUENCE: 2.11

SEQUENCE: SEGUENCE: 2.11
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA

RORANISH: Homo sapiens
FEATURE:
NAME/KEY: gource
LOCATION: (1)..(4319)
FEATURE:
NAME/KEY: CDS
LOCATION: (301)..(308)
FEATURE:
NAME/KEY: CDS
LOCATION: (3128)..(3531)
FEATURE:
NAME/KEY: CDS
LOCATION: (3660)..(4119)
FEATURE:
NAME/KEY: CDS
LOCATION: (3660)..(4119)
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(48)
COTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1619
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                                                                                                                                                                                                                                   CCCCTCATGGTCCTGGTGCCCTTTGCCATTGGCTTCTGTGGGCCAGTGGGGATCATCCTG
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| Sequence 40. Application US/09728952
| Patent No. US20020111302A1
| GENERAL INFORMATION:
| APPLICANT: Tang, Y: Tom
| APPLICANT: Goodrich, Ryle
| APPLICANT: Goodrich, Ryle
| APPLICANT: Hand; Vinod
| APPLICANT: Wang, Dunrui
| APPLICANT: Wang, Dunrui
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37.0%; Score 409; DB 9; I
Best Local Similarity 99.7%; Pred. No. 9.8e-199;
Matches 579; Conservative 0; Mismatches 1;
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; LOCATION: (684)..(1016)
US-09-728-952-40
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ORGANISM: Homo sapiens
FEATURE:
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US-09-728-952-40
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Sequence 1293, Application US/10292798

Sequence 1293, Application US/10292798

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASMATIKA, YUTAKA,
APPLICANT: ABURATANI, HIROYUKI
FILE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT FILING DATE: 2002-11-13
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-6-18
NUMBER OF SEQ ID NOS: 2070
SEQ ID NOS: 2070
SEQ ID NO 1293
LENGTHE: A319
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41.8%; Score 461; DB 15; Length 4319;
Best Local Similarity 99.8%; Pred. No. 2.3e-225;
Matches 581; Conservative 0; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                     3479 TCCTGCTATATGAAGATCACCTGGAAGCTGTGCAGACACAGCT 3520
                                                                                                                                                                                                                                                                      637 TCCTGCTATATGAAGATCACCTGGAAGCTGTGCAGCACAGCT 678
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ORGANISM: Homo sapiens
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| Sequence 64, Application US20040014169A1
| GENERAL INFORMATION:
| APPLICANT: Wogel; Gabriel
| APPLICANT: Wogel; Gabriel
| APPLICANT: Wogel; Gabriel
| APPLICANT: Wogel; Gabriel
| APPLICANT: Wogel; Gabriel
| APPLICANT: Wogel; Gabriel
| APPLICANT: Wogel; Gabriel
| FILE REFRENCE: 00100031
| FILE REFRENCE: 00100031
| CURRENT APPLICATION NUMBER: US/09/801,944B
| CURRENT APPLICATION NUMBER: 60/187,715
| PRIOR APPLICATION NUMBER: 60/187,715
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR PELLORICATION NUMBER: 60/187,930
| PRIOR PELLORICATION NUMBER: 60/187,930
| PRIOR PELLORICATION NUMBER: 60/187,930
| PRIOR PELLORICATION NUMBER: 60/187,930
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| PRIOR PELLORICATION NUMBER: 60/187,581
| PRIOR PELLOR NUMBER: 60/187,581
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| PRIOR PELLOR DATE: 2000-03-08
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NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
SEQ ID NO 64
LENGTH: 556
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Pred. No. 1.8e-79;
0; Mismatches 1;
PRIOR APPLICATION NUMBER: 60/194, PRIOR FILING DATE: 2000-04-03 PRIOR PILING DATE: 2000-07-14 PRIOR FILING DATE: 2000-07-14 NUMBER OF SEQ ID NOS: 184; SOFTWARE: Patentin version 3.0 SEQ ID NO 35 LENGTH: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6%;
Matches 226; Conservative
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, ORGANISM: Homo sapiens
US-09-791-932-35
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CORGANISM: Homo sapiens
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N BOND MARKOW, SIGNAL = 3.1
N LUNG, SIGNAL = 2.8
N HELA, SIGNAL = 2.8
N HELA, SIGNAL = 3.3
N HEART, SIGNAL = 3.3
N PLACENTA, SIGNAL = 3.7
N PLACENTA, SIGNAL = 3.7
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                                                              PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00669
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                                                 US 09/632,366
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ORGANISM: Homo sapiene
PEATURS:
OTHER INFORMATION: EXPRE
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Matches 31
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Betent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR FILE REPRENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

FRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Robison, Keith E
TITLE OF INVENDION: NO. US20020055179Alel G-Protein Coupled Receptor Homologs
TITLE OF INVENDION: NO. US2002005183478
CURRENT APPLICATION NUMBER: US/09/812,102
CURRENT APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
RIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 90
LENGTH: 594
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                                                                                                                                                                                                                                                                                                   496 GIGGICIAGCITCAGCCCTACCACCICAACAICAAGCAGTICAIGGCGAGAGGIAIGCTC 437
                                                                                                                                                                                   556 AGCAGGAAAGGACGCCACTGGCGAGGCTGCCTTACGCTGATGCTGATGCTGGTGGCCGTG 497
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                                                                                                                                                                                                                                                 757 GIGGICIGCIICAGCCCCIACCACCICAAGAGGAGGAGGAGGGAIGCIC
                                                                                                                            697 AGCAGGAAAGGACGCCACTGGCGAGGCTGCTTACGCTGCTGATGCTGGTGGCCGTG
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      Score 159; DB 11; Length 556;
Pred. No. 9e-71;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                877 CTCATGAACATGAACTGTGGCATTACCCCA 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 90, Application US/09812102
Patent No. US20020055179A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: GPCR-RHODOPSIN US-09-812-102-90
Query Match
Best Local Similarity 99.5%;
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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US-09-812-102-90/c
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APPLICANT: KTEQE, JOICHAN
APPLICANT: FUGURATION OF PROPERTY, NICHOLAS
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PLING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1941
                                                                                                                                                                                                                                                                                                                                    GENERAL INCOMENTATION:

APPLICANT: Budworth, Paul R.

APPLICANT: Briggs, Steven P.

APPLICANT: Cooper, Steven P.

APPLICANT: Cooper, Briggs, Stephen A.

APPLICANT: Gazebrock, Jane

APPLICANT: Gazebrock, Jane

APPLICANT: Gargiri, Fumiyaki

APPLICANT: Katagiri, Fumiyaki

APPLICANT: Katagiri, Fumiyaki

APPLICANT: Katagiri, Nicholas

APPLICANT: Ricke, Darrell

APPLICANT: Ricke, Darrell

APPLICANT: Ricke, Darrell

APPLICANT: Ricke, Darrell

APPLICANT: Ricke, Darrell

APPLICANT: Ricke, Darrell

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APPLICANT: Ricke, Darrell

APPLICANT: Ricke, Darrell

APPLICANT: SOUROPERS FOR REGULATION OF PLANT EXPRESSION

FILE REFERENCE: 60111-NP

CURRENT APPLICATION NUMBER: US 60/325,448

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

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2.8%; Score 31; DB 15; I
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972 GICTICCICCICCICCICCICCICCICCICCICC 1002
                         327 Trecreterecreterecreterecreter 357
                                                                                                                                                                                                                   Sequence 5532, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
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Moughamer, Todd G.
Briggs, Steven P.
Cooper, Bret
Glazebrook, Jane
Goff, Stephen A.
Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fumiyaki
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; ORGANISM: Zea mays
US-10-260-238-5532
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APPLICANT: Hanzel, David K.
APPLICANT: Chem, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICHORARAY
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICHORARAY
CURRENT APPLICATION NUMBER: US/09/644,761

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

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LALE NARROW, SIGNAL = 3.1.

LALERSSED IN BRAIN, SIGNAL = 2.8

LON: EXPRESSED IN HELA, SIGNAL = 3.3

ON: EXPRESSED IN HEART, SIGNAL = 7.

N: EXPRESSED IN PLACENTY

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T: EXPRESSED IN UT-
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ADULT LIVER, SIGNAL
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ORGANISM: Homo sapiens
FEATURE:
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US-10-029-386-17166
US-10-029-386-17166
Sequence 17166, Application US/10029386
Sequence 17166, Application US/20030194704A1
Sequence 17166, Application No. US20030194704A1
Sequence 1716ANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANTON: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17166
ILENGRAPH: 180
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN PRAIN, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 0.71
OTHER INFORMATION: BY HUXAN HIT: A1863660.1, FVALUE 6.30e+00
OTHER INFORMATION: NT HIT: AF059679.1, EVALUE 4.30e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%; Score 30; DB 9; Length 123; 100.0%; Pred. No. 0.0001; tive 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORWATION: MAP TO CHR22 184 2.0
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
                                                                  PRIOR APPLICATION NUMBER: PCT/USO1/00664

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR APPLICATION NUMBER: PCT/USO1/00669

PRIOR APPLICATION NUMBER: PCT/USO1/00665

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/USO1/00663

PRIOR APPLICATION NUMBER: PCT/USO1/00663

PRIOR APPLICATION NUMBER: PCT/USO1/00663

PRIOR APPLICATION NUMBER: PCT/USO1/00662

PRIOR APPLICATION NUMBER: PCT/USO1/00662

PRIOR PLICATION NUMBER: PCT/USO1/00661

PRIOR PLICATION NUMBER: PCT/USO1/00670

PRIOR PLICATION NUMBER: PCT/USO1/00670

PRIOR PLICATION NUMBER: US 60/234,687

PRIOR PLICATION NUMBER: US 99/608,408

PRIOR PLICATION NUMBER: US 09/608,408

PRIOR PLICATION NUMBER: US 09/774,203

PRIOR PLICATION NUMBER: US 09/774,203

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PRIOR PLICATION NUMBER: US 09/774,203

PRIOR PLICATION NUMBER: US 09/774,203

PRIOR PLICATION NUMBER: US 09/774,203

PRIOR PRIOR DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SEQ ID NO 27614
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Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPRENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-04
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100.0%; Pred. No. 2.7e-05;
tive 0; Mismatches 0; Indels
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APPLICANT: YANASHITA, ICHIRO
TITLE OF INVENTION: High espensabilive medaka fish
TITLE OF INVENTION: High espensabilitive medaka fish
FILE REPERENCE: 21021705-620-7249-0
CURRENT APPLICATION NUMBER: US/09/893,666A
CURRENT PILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 10 2000-247729
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
LENGTH: 2764
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2.8%; Score 31; DB 15; L
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Patent No. US20020048763A1
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; LOCATION: (211)..(1935)
; OTHER INFORMATION:
US-09-893-666A-1
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1941
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US-09-864-761-27614
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US-09-893-666A-1/c
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EXPRESED IN LUNG, SIGNAL = 2.8

EXPRESED IN HELA, SIGNAL = 3.1

EXPRESED IN HERAT, SIGNAL = 2.5

EXPRESED IN HERAT, SIGNAL = 2.5

EXPRESED IN FORTAL LIVER, SIGNAL = 2.7

EXPRESED IN FORTAL LIVER, SIGNAL = 2.3

NT HIT: AF020931.1, EVALUE 4.90e-01

EST_HUMAN HIT: AA703592.1, EVALUE 7.30e-01
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Patent No. US20020048763A1
Patent No. US20020048763A1
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Horsel, David R.
APPLICANT: Gene BENERONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US 909/864,761, CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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                   CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8 CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9 CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6 CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.8 CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2 US-10-029-386-17166
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: 3000-05-26
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SOFTWARE: Annomax Sequence
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BONLU34TR BOMMY77TF

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BH542697 CD845470 CD845470 CD845620 BH667864 BH667361 BH67361 BH67361 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 BH770613 CD7230907 CD73007 CD73007 CD73007 CD73007 CD73007 CD73007 CD73007 CD73007 CD73007 CD73007 CD73007

Fetraodon

RPCI-24-3 QCU17g11. RPCI-23-3 3529_1_37 GG5EA46TV hp78f08.b SCCCFL409 SCSEAD108

PUIDV14TB OG5CH40TC PUFYW39TB

Tetraodon

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Tetraodon

Title: Perfect score:

Sequence:

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Scoring table:

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Database :

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 594)

Noti-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

L Onpublished (1997)

Contact: Robert. Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov)

This clone is available royalty-free through LLNL; contact the Infactone is available royalty-free through LLNL; contact the Infactone is available royalty-free through LLNL; contact the Infactorium (info@image.llnl.gov) for further information.

Insert Length: 10.4 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 408.

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CF063130
AZ039077
CB33456
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CB079907
CA235347
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AB055167
CB668345
CNS04PSZ
CG047970
CG253509
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CG026240
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Homo sapiens (human)
RESULT 1
A1659965/c
LOCUS
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                                               togers, J., Birney, E. and Hayashizaki, Y.
that ye is of the mouse transcriptome based on functional annotation
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/lab_host="DH10B (phage-resistant)"
                     /clone="IMAGE:2345880"
/mol type="mRNA"
/db xref="taxon:9606"
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Mus musculus
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Contact: Yoshihide Hayashizaki

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-922

Fax: 81-45-503-921

Fax: 81-45-503-921

Full: prome-res@gsc.riken.go.jp,

Will:http://genome-gsc.riken.go.jp,

Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Muraca,M., Nakamura,M., Nounua,K., Numazaki,R.,

Ohno,M., Sakai,K., Sakazume,M., Sasaki,D., Sato,K., Shibata,K.,

Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and

Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared

Normalization and subbraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Reg. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence din Rosearch Group in Riken

Conductor and subpermed and sequenced in Mouse Genome

Encyclopedia project of Genome Exploration Research Group

Division of Experimental Animal Research in Riken contributed to
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bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/clone_lib="RIKEN full-length enriched, whole joints"
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Local Similarity 100.0%; Pred. No. 7.2e-06; les 34; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:10090"
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BH542697 271 bp DNA linear GSS 14-DEC-2001
BOHLP40TR BOHL Brassica oleracea genomic clone BOHLP40, genomic
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Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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/mol_type="genomic DNA"
/db strain="TOJ000DH3"
/db strain="toJ000DH3"
/clone="BOHLP40"
/clone lib="BOHL"
/note="Wector: pHOS1, Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 271)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

Other GSSs: BOHLP40TF

Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-3523

Fax: 301-838-0208

Email: cdrowdigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1. 271

/organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%; Score 32; DB 10;
100.0%; Pred. No. 8.5e-05;
live 0; Mismatches 0;
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                     Location/Qualifiers
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BH542697
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POLYA=Yes
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Conduct: Soares, MB
Coordinated Laboratory for Computational Genomics
University of lowa
375 Newton Road, 4156 MEBRF, lowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8250
Email: bence-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the Notl site and the Oligo-dT track served to verify it as a a clone from the non-normalized embryo at 13 dpc library CDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this CDNA sequence: 4-123,
(GAA)n#Simple repeat 143-240, >162_Send#LINE/Li
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW532693 240 bp mRNA linear BST 06-MAR-2000 UI-R-BSO-amg-a-06-0-UI.sl UI-R-BSO Rattus norvegicus cDNA clone UI-R-BSO-amg-a-06-0-UI 3', mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/note="Vector: pHoS1; Site 1: BstX1; 2-3 kb sheared
genomic DNA inserted into pHoS1 using BstX1 linkers"
                  Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other GSSs: BOWHESTIF
Contact: Chris Town
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0
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                 TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                | organism="Brassica oleracea"
| mol_type="genomic DNA"
| strain="r01000BH3"
| db_xref="taxon:3712"
| clone="BOMHB51"
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BZ499662
BONLU34TR BO 1.6_2_KB_tot Brassica oleracea genomic clone BONLU34, genomic survey sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae; Brassica.
1 (bases 1 to 539)
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Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Fax: 33 169 47 54 00
Fax: 33 169 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infoblogen.fr)
Location/Qualifiers
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                                                   | 1.507 | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contact | Contac
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/mol_type="mRNA"
/culfivaz="asmourai" (restored line)"
/db_xref="taxon:3708"
/clone="RF02119118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%; Score 32; DB 14; I 100.0%; Pred. No. 9.6e-05; ive 0; Mismatches 0;
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/clone_lib="RF02"
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Matches 32; Conserva
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RFO2.115J02F010530 RFO2 Brassica napus CDNA clone RFO2115J02, mRNA
sequence.
                                                                                                                                                                                                                                                        CUP45470 SFO2 143F14F011228 RFO2 Brassica napus CDNA clone RFO2143F14, mRNA sequence.
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Wharyora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 506)
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Contact: Genoplante
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fax: 33 logary contact generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
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Genoplante, a major partnership french program in plant genomics Unpublished (2003)

Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/clone="RF02143F14"
/tissue type="anthers"
/clone_lib="RF02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               973 TCTTCCTCCTCCTCCTCCTCCTCCTCCAC 1004
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Gaps ô

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

LOCUS

RESULT 7 CD839500

à d us-10-041-615-33.oli10.rst

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genomic DNA inserted into pHOS1 using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
                                                                                                                                                 Length 613;
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Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 32; Conservative 0; Mismatches 0;
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2.9%; Score 32; DB 28; L
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 32; Conservative 0; Mismatches 0;
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Fax: 301-838-0208
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                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Brassica. 1 (bwn.C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Other GSSs: BONIU314TF
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
I (bases II; Brassicales; Brassicaceae; Brassica.
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Unpublished (2001)
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dlone lib="BO 1.6 2 KB tot"
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total DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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100.0%; Pred. No. 9.7e-05;
ive 0; Mismatches 0; Indels
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Tel: 301-838-3523
Fax: 301-838-0208
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/clone="BONLU34"
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   BZ499662
BZ499662.1 GI:27014967
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BONAF76TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONAF76, genomic survey sequence.
BZ430821.1 GI:26676292
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
I cosida; eurosida II; Brassicales; Brassicaceae; Brassica.

Town,C.D., Van Aken,S., Utterback,I., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Gaps
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genomic DNA inserted into pH051 using BstXI linkers"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Cosids; eurosids; Brassicales; Brassicaceae; Brassica.

(bases 1 to 701)
Delehannty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Mah,W., Rabinowa,Cz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
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Brassica oleracea
Brakaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Wholls genome shocgun sequencing of Brassica oleracea Unpublished (2001)
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Fax: 301-838-0208
Email: cdtown@tigr.org
MA is firm a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
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100.0%; Pred. No. 9.9e-05;
ive 0; Mismatches 0; Indels
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Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odh46 row: a column: 04
Seq primer: -21UPpOT forward
Class: shorgun
High quality sequence start: 65
High quality sequence stop: 474.
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    /organism="Brassica oleracea"

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High quality sequence start: 18
High quality sequence stop: 551.
High quality sequence stop: 551.

Liocation/Qualifiers

1. .702

/organism="Brassica oleracea"
/mol type="genomic DNA"
/db_xref="taxon:3712"
/dlone lib="B.oleracea002"
/note="vector: pOTw12"
/note="vector: pOTw12"
/note="vector: pOTw12"
/note="vector: pOTw12"
/notes buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 702)

Bases I to 702)

Nash, W., Fabinowicz, P.D. and Wilson, R.K.

Nash, W., Rabinowicz, P.D. and Wilson, R.K.

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Wabhington University School of Medicine

Email: submissions@watson.wustl.edu

Plate: odf67 row: h column: 07

Seg primer: -21UPPOT forward

Class: shotgun
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AZO3.101K13F010928 AZO3 Triticum aestivum cDNA clone AZO3101K13, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH918360 702 bp DNA linear GSS 01-OCT-2002 odf67h07.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
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flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Misconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Shotgun ibrary prepared at Washington University Genome Sequencing Center."
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                                                                                                                                                                                                                                   Score 32; DB 28; Length 701; Pred. No. 0.0001; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.9%; Score 32; DB 28; Length 70
100.0%; Pred. No. 0.0001;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. v..
0; Mismatches
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VERSION CD874215
VERSION CD874215.1 GI:32558031

KEYMORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum (bread wheat)

SOURCE
Triticum aestivum (bread wheat)

Triticum aestivum (bread wheat)

REFERENCE | Lobese | Triticum aestivum |
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Boideae; Triticum |
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Search completed: February 21, 2004, 23:44:56 Job time : 2815 secs

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February 19, 2004, 19:17:05; Search time 43 Seconds (without alignments) 1328.874 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect :
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RIES	Description	6 Human GPCR16 prote								
SUMMARIES	QI	ABG3228	ABG14682	AAR5408	AAW5362	AAY90630	ABP8181	AAY9066	ABG6669	AAU25588
	DB	23	22	15	19	21	24	21	23	22
	% Query Match Length DB	360	377	361	361	361	361	361	110	177
	% Query Match	100.0	80.3	33.7	33.7	33.7	33.7	33.6	29.6	22.2
	Score	1876	1506	632.5	632.5	632.5	632.5	630.5	555	417
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03-JAN-2001; 2001US-259552P. 09-JAN-2001; 2001US-260544P. 20-MAR-2001; 2001US-277405P. 03-JAN-2002; 2002WO-US00056

110	95.5	20.9	339	15	AAY90652 AAR53752	
ന ന	91.	20.0 0.0	თ თ ო ო ო ო	1 18 6 6	AAW07617 AAW48733	Human G-protein th Human R12 seven tr
m	91.	20.9	339	21	AAB21697	
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m	91.	20.9	338	22	AAB82853	
m	91.	20.9	339	23	AAU98065	Ü
m	91.	20.9	339	23	AAU91239	Human 7 transmembr
m	91.	20.9	339		ABU11906	Human G-protein co
m	91.	20.9	367		ABP81909	Human G protein-co
m	77.	20.1	177		AAU19222	Human G protein-co
	355	18.9	371		ABG35299	type
m	52	18.8	402		ABG35298	Human PAR1 type th
m	52.	18.8	425		ABG35300	
	340	18.1	425		AAR60698	Fragment of the hu
m	39.	18.1	425		AAR27240	thrombin
m	39.	18.1	425		AAW51407	protease-
m	39.	18.1	425		AAY49570	
m	39.	18.1	425		AAG80697	Human thrombin pro
m	39.	18.1	425		AAE17032	thrombin
m	39.	18.1	425		ABR47449	Breast cancer asso.
m	39.	18.1	425		ABP81919	Human thrombin rec
m	39.	18.1	425		ABG73511	Human thrombin pro
m	39.5	18.1	426		AAY45035	Human thrombin rec
m	39.	18.1	892	8	AAW16314	Human thrombin rec
m	32.	17.7	420	24	ABG73510	X. laevis thrombin
	332	17.7	537	23	AAU74538	Human P2Y purinoce
	331	17.6	328	17	AAR91225	Human placenta G-p
	329	17.5	328	22	AAE04393	Human P2-purinergi
	329	17.5	328	24	ABP81869	Human purinergic r
	328	17.5	355	22	ABB56343	Non-endogenous hum
	324	17.3	328	78	AAW09433	Human placenta pur
	324	17.3	355	₩	AAW07618	Human G-protein re
	324	17.3	355	19	AAW49807	Human G-protein ch
	324	17.3	355	20	AAW97868	Human CC chemokine

ALIGNMENTS

ABG32286 standard; Protein; 360 AA.

RESULT 1 ABG32286 ABG32286;

cardiomyopathy; atherosclerosis; diabetes; cancer; stroke; Von Hippel-Lindau syndrome; Alzheimer's disease; tuberous sclerosis; Non Hippel-Lindau syndrome; Alzheimer's disease; tuberous sclerosis; hypercalcaemia; Parkinson's disease; furtington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; addiction; anxiety; depression; pain; obesity; Crohm's disease; osteoporosis; haemophilia; asthma; inflammatory bowel disease; infertility; hypertension; scleroderma; arthritis; human immunodeficiency vius; autoimmune disease; HIV; infection; graft-versus-host disease. G protein coupled receptor related protein; human; GPCR; (first entry) Human GPCR16 protein. WO200264793-A2. Homo sapiens. 15-NOV-2002 22-AUG-2002.

```
This invention relates to a new isolated G-protein coupled receptor

(GPCRX) polypeptide, acid and an antibody specific to the protein
are useful for treating, preventing an antibody specific to the protein
are useful for treating, preventing or alleviating a GPCRX-associated
disorder or a pathological state in a subject, particularly a human. In
pairtcular, the disorder is cardiomyopathy, atherosclerosis, diabetes,
or a disorder related to cell signal processing and metabolic pathway
or medicanearit for prevential processing and metabolic pathway
cc diagnosing the presence of or preddsposition to a disease associated
with altered levels of GPCRX, particularly cancer. The GPCRX nucleic
with altered levels of GPCRX, particularly cancer. The GPCRX nucleic
cc acid and polypeptide are especially useful in the manufacture of a
medicament for therapeutic or prophylactic applications for disorders
associated with aberrant GPCRX syrression or activity, e.g. von
Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous
cc atomic obseits, puppercal caemia, Parkinson's disease,
sclerosis, hypercal caemia, Parkinson's disease,
creebral palsy, epilepsy, Lesch-Wyhan syndrome, multiple sclerosis,
disease, infertility, hypertension, scleroderma, haemophilia,
athmitis, human immunodeficiency virus; autoimmune disease,
for treating the above conditions. The polypeptides can be used as
the disease. The DNA encoding the protein is useful in gene therapy
for treating the above conditions. The polypeptides
consumnosens to produce antibodies and as vaccines of the nucleic acids are
further used as hybridiastion probes, in chromosome mapping, tissue
typing, preventive medicine, and pharmacopennous. The puseful
in developing powerful assay system for functional analysis of various
consumers are presented and protein coupled receptor related protein
consumence represented and hybridiastion protein coupled receptor related protein
consumence are processed as hybridiastion probes, in chromosome mapping, the protein
consumence are proc
                                                                                                                                                                                                                                   New isolated G protein coupled receptor polypeptides and polynuclectides, useful in gene therapy, particularly for treating or preventing cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
                                                                           Ellerman K, Smithson G,
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 98; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GPCR) of the invention.
                                                                              Edinger SR,
                          (CURA-) CURAGEN CORP.
                                                                                                                                                          WPI; 2002-643487/69.
                                                                                                                                                                                          N-PSDB; ABS64723
                                                                                                        Muralidhara P;
                                                                              Casman SJ,
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360 AA; Sequence

Gaps ; 0 Query Match 100.0%; Score 1876; DB 23; Length 360; Best Local Similarity 100.0%; Pred. No. 2.1e-191; Matches 360; Conservative 0; Mismatches 0; Indels 0;

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MEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR 181 181

GCLLTLLMLVAVVVCFSPYHLNIKQFWARGMLHLPSCAERRAFLLSLQATVALMNMVCGI

241

301 TPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSSTPGKASSETPSITQARGSMFLAEHVV

RESULT 2 ABG14682

Kekuda R;

ABG14682 standard; Protein; 377

Æ.

ABG14682;

18-FEB-2002 (first entry)

Novel human diagnostic protein #14673.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC

Tang YT; riu c, Drmanac RT,

WPI; 2001-639362/73.

N-PSDB; AAS78869.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 20; SEQ ID No 45041; 103pp; English.

The invention relates to isolated polynucleotide (1) and probes, polymeride (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome configuration of (11). The polymucleotides are also used in diagnostics as expressed sequence tags for the infinity expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving to restore normal activity of (11) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a fool osupplement. (11) and its binding partners are useful in medical inaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention.

377 AA; Sequence

240

Gaps 4; Indels 66; 80.3%; Score 1506; DB 22; Length 377; 80.6%; Pred. No. 6.8e-152; ive 1; Mismatches 4; Indels 66; Matches 295; Conservative Local Similarity Query Match

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94 DEVIALLVESALGNILALCLTCQKSEKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGS 35

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92US-0980518
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25-NOV-1992;
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                                                                          224
                                                                                         190 YMXITWKLCSTAGRIQXPAGKDTTGGASPGGPSDQPEKTPPAGAAQEDPVTPRERTPPAG 249
                                                                                                                 250 QPERTQXPAGKDATGGTAREDPVISRKGRHWRGCLLILILIMIVAVVVCFSPYHLNIKQFMA 309
                                                                                                                                     RGMLHLPSCAERRAFLLSLQATVALMNWNCGITPIIYFFASTHYRKWLLGILKLKGSSSS 328
69
                                                                                                                                               LFYTALLVFSALGNILALCLTCQKRRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGS
               SWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAI
                        WILVILQIMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSC
                                                                                                        -----TAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFMA
                                                                                                                                                                                                                                                                                                                                                                                                                 conserved among a large number of G-protein coupled receptors."
                                                                                                                                                                                                                                                                                                                                                       'note= "Potential N-linked glycosylation site."
                                                                                                                                                                                                                                                                                         Epstein Barr virus; EBV; induction; detection; diagnosis; lymphocytes; antigen; growth; differentiation; mediator; infectious mononucleosis.
                                                                                                                                                                                                                                                                           Epstein Barr virus induced (EBI-2) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                  "This sequences motif
(S-[I/V]-D-R-[Y/F]-X
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Label= Hydrophobic region.
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/label= Hydrophobic region.
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/label= Hydrophobic region.
126..134
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/label= Hydrophobic region.
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/label= Hydrophobic region.
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/label= Hydrophobic region.
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                                                                                                                                                                                                                        AAR54080 standard; Protein; 361 AA.
                                                                          AWKI TWKICS------
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(first entry)
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Modified-site
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03-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 MEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 INLGPYFTPPTKI-KTKIKDLNVESOTVKIFLRSLFYTALLVFSALGNILALCLTCOKSR
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                                                                                                                                                                                                                                                                                                                                                                                                               BBV infected B lymphocytes recapitulate features of antigen stimulation in enlarging, increasing RNA synthesis, expressing activation antigens and adhesion molecules, secreting Ig and proliferating. Unlike antigens etimulated B lymphocytes, BBV infected B lymphocytes continue to proliferate (in vitro) as immortalised lymphoblastoid cell lines. Because of the similar effects of EBV and antigen, EBV induced genes are likely to include mediators of antigen induced B lymphocyte growth or differentiation. (Updated on 25-WAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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33.7%; Score 632.5; DB 15; Length 361;
Best Local Similarity 37.8%; Pred. No. 1.1e-58;
Matches 135; Conservative 74; Mismatches 141; Indels 7;
                                                                                                                                                                                                                   DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s) and antibodies to EBI1, 2 and 3 - useful for detecting EBV by hybridisation or by immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epstein Barr virus induced gene 2 (EBI-2).
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                                                                                                                                                                                                                                                                                                                                                     8; Page 58-60; 84pp; English.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
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                                                                Birkenbach M, Kieff
                                                                                                                              WPI; 1994-200183/24.
N-PSDB; AAQ64126.
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Homo sapiens

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MEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 GITPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSSTPGKAS---SETPSITQARGS 352
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                                                                                                                                                                                                       Assessing or monitoring foetal or placental development - comprises detecting the level or size of Epstein Barr virus induced nucleic acid or protein in maternal serum samples
                                                                                                                                                                                                                                                                                      The present sequence was used in the development of a novel method for assessing or monitoring foetal or placental development. The method comprises taking a maternal serum sample, and detecting the level or sizé of Epstein Bark virus (EBV) induced gene or protein 3 (EBI-3) to obtain a result, which can be compared to a control to assess or monitor foetal or placental development.
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 632.5; DB 19; Length
37.8%; Pred. No. 1.1e-58;
tive 74; Mismatches 141; Indels
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                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL
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                                                    95US-0383750.
92US-0980518.
94US-0352678.
                            95US-0383750
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                                                                                                                                       Birkenbach M, Kieff
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es 135; Conserva
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N-PSDB; AAV25491.
                                                                                                                                                                                                                                                                                                                                                                                          361 AA;
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                            02-FEB-1995;
                                                                                  30-NOV-1994;
 28-APR-1998
                                                        02-FEB-1995
                                                                      25-NOV-1992
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRS, AAY90643-CAAY90677 and AAA30779-A30773 and AAA30779-A30779). The mutant proteins of the invention contain a and AAA30779-A30779). The mutant proteins of the invention contain a contain a portion of the protein comprising intracellular loop 3 (CO3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence of a substituted for an endogenous maino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this or Ala, and is preferably Lys. When the substituted amino acid and the Process of a modern or an anix or a mixture of endogenous and may be endogenous, non-endogenous, or a mixture of endogenous and con-endogenous, non-endogenous, or a mixture of endogenous and partial agonists for use as particular grounds the roles of the receptors in normal and partial agonists for aluidating the roles of the receptors in normal and settings for aluidating the roles of the receptors in normal and discorders as associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be useful for the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous and incenting of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
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Best Local Similarity 37.8
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                               (AREN-) ARENA PHARM INC
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                                                               40200022129-A1
                                                                                                                                                                                               12-OCT-1999;
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4.

120

61

61.

The present invention describes antigenic peptides (I) comprising:

(a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular of protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific an inclody against a particular GPCR, and in the production of specific an inclody against a particular GPCR, and in the production of specific an antibodies. The peptides and antibodies are useful for disagnosting one descriping for gresence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for disagnosting and designing drugs for treating immune-related diseases, immunological-related diseases, coll regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, costeoarthritis, osteoprosis, ancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, pain, psoriasis, considers anxiety, depression, schizophrenia, dementia, member, peraves host disease, elementia, perepagance, perepagance, or anxiety, depression, schizophrenia, dementia, mental retardation, memory consistention, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; Annew disease; atheroscient disease; autoimmunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroscierosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, GITPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSSSTPGKAS---SETPSITQARGS 352 302 CMDPFIYFFACKGYKRKWMRMLKRQUSVSISSAVKSAPEENSREMTETQMMTHSKSS 358 Human EBV-induced gene 2 protein SEQ ID NO:112. Disclosure, Fig 1; 523pp; English. ABP81814 standard; Protein; 361 AA (LIFE-) LIFESPAN BIOSCIENCES INC. Burmer GC, Roush CL, Brown JP; cancer or autoimmune diseases 19-DEC-2001; 2001WO-US50107. 19-DEC-2000; 2000US-257144P. 04-MAR-2003 (first entry) WPI; 2003-046718/04. N-PSDB; ABZ42660 WO200261087-A2 Homo sapiens, 08-AUG-2002 ABP81814; ulcer. RESULT 6

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MACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLLMPWTKPLVGKLAC 180
                                                                                                                                                                                                                                                                                    181 MEYSSMESVLGLPLMVLVAFALGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR 240
                                                                                                                                                                                61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGYYL 120
                                                                                                                                                                                              62 KINSTLLYSTNLVISDILETTALPTRIAYYAMGFDWRIGDALCRITALVFYINTYAGVNF 121
                                                                                                                                                                                                                                                                                                     242 ALWIILLIIVVEVLCETPYHVALIQHMIKKCLRESNFLECSQRHSFQISLHFIVCLMMFNC 301
                                                                                                                                                                                                                                                                                                                                                                                                           302 CMDPPIYFFACKGYKRKVWRMLKRQVSVSISSAVKSAPBENSREMTETQMMIHSKSS 358
                                                                                                                                                                                                                                                                                                                                                                                             299 GITPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSSTPGKAS---SETPSITQARGS 352
                                                                                                                                             241 GCLLTLIMIVAVVVCFSPYHLNIKQFMARGM--LHLPSCAERRAFLLSLQATVALMNMNC
                                                                                                                              2 IKLGPYFTPPTKI-KTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR
used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents
                                                                                                    7;
                                                                           33.7%; Score 632.5; DB 24; Length 361; 37.8%; Pred. No. 1.1e-58; ive 74; Mismatches 141; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mutant G protein-coupled receptor EBI2 (1243K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 262-263; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY90664 standard; Protein; 361 AA
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                                                                                                        Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-329165/28.
N-PSDB; AAA30730.
                                                                                           Best Local Similarity
                                                       361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
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fungal infection.

Homo sapiens.

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-C AAY90677 and AAA30779-A307743 and to DNA encoding them (AAA30779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous anno acid, X, cisubstituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence of acids N-terminal of an endogenous amino acid is selected from Lya, His, Arg or Ala, and is preferably Lya. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promay be endogenous. In on-endogenous, or a mixture of endogenous and on-endogenous and partial agonists for use as identifying antagonists, agonists and partial agonists for use as planamaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used the novel mutant GPCRs are constitutively active, they can be used constitutions. Antagonists AAY90677 and AAY90683-Y90687 the mutant constitution.
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361 AA; Sequence

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181 MEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR 240
                                                                                                                                                                                                                                                                                                                              241 GCLETLIMIVAVVVCFSPYHINIKOFMARGM--LHLPSCAERRAFILISLOATVALMNMNC 298
                                                                                                                                                  61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
                                                                                                                                                                        62 XINSTILYSTRIVISDILFTTALPTRIAYYANGFDWRIGDALCRITALVFYINTYAGVNF 121
                                                                                                                                                                                                                            MACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLAC 180
                                                                                                                                                                                                                                                        242 AKNTILLIVVVFVLCFTPYHVAIIQHMIKKLRFSNFLECSQRHSFQISLHFTVCLMNFNC 301
                                                                        2 IKLGPYFTPPTKI-KTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR 60
                                                                                                            3 İQMANNFİPPSATPQGNDCDLYAHHSİARİVM-PLHYSLVFIIGLVGNLLALVVIVQNRK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 GITPILYFFASTHYRKWLLGILKLKGSSSSSSSSSSTPGKAS---SETPSITQARGS 352
                                          Gaps
                                        7
    DB 21; Length 361;
33.6%; Score 630.5; DB 21; Length
37.8%; Pred. No. 1.8e-58;
tive 74; Mismatches 141; Indels
                          Local Similarity 37.8
hes 135; Conservative
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        Query Match
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Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyoricophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelat disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
                  ABG66698 standard; Protein; 110 AA.
                                                                                                                                                   Human novel polypeptide #33.
                                                                                                       (first entry)
                                                                                                         30-AUG-2002
                                                                 ABG66698;
ABG66698
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AAU25588 standard; Protein; 177 AA

18-DEC-2001

AAU25588;

AAU25588 ID AAU2 XX AC AAU2 XX DT 18-E

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The invention relates to human novel polymucleotides and associated colypeptides. The polymucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephrities, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and respensation of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, parkinson's disease, Huntington's disease and amyotrophic lateral.

Crossis: The sequences are involved in chemotactic or chemokinetic activity, regulation of hasmatopolesis, treatment of myeloid or lymphoid cut disorders and platelet disorders such as thrombostyopenia, cell disorders and platelet disorders such as thrombostyopenia, cell disorders and platelet disorders such as thrombostyopenia, cell such activity, regulation of bone, our artilage, tendon, ligament and/or nerve tissue crossis, osteoarthritis, bone degenerative disorders in and pariodontal cyprection or regeneration and treatment of lung or liver fibrosis, concention or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiency (SCID), bacterial or fibrogic influding sevener combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders eq. multiple sclerosis and mysathenia conditions such as asthma, thrombolysis or thrombosis and now inverviewed the invention injurer inventions of the invention are also threamed the and an expresent human and the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the propertion of the invention of the invention of the invention of the invention of the propertion of the inv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 555; DB 23; Length 110;
Pred. No. 4.3e-51;
0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                       ה,
                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides for diagnosis,
                                                                                                                                                                                                                                                                                                                                       Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory, autoimmune, nervous system, myeloid disorders, cancer and promoting wound healing -
                                                                                                                                                                                                                                                                                                                                       Liu C, Zhou P,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel polypeptides of the invention.
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Best Local Similarity 99.1%;
Matches 105; Conservative
                                                                                                                                                                                            30-NOV-2001; 2001WO-US47004.
                                                                                                                                                                                                                                         10-NOV-2000; 2000US-0028952.
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Yamazaki V, Ujwal ML,
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                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                              40200244340-A2.
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us-10-041-615-34.rag

161 OTMPLILIMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITW 220

221 KLCST----

g 8 8 AAY90652 standard; Protein; 339 AA

RESULT

AAY90652;

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Page

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Sequences AAU25554-AAU25616 represent human G-protein coupled receptor (GPCR) polypeptides of the invention. The proteins and their associated boly sequences can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, a GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such amitangological disorders such as obseity, anorexia and type 2 diabetes, cardiovascular disorders such as thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis, viral infections caused by HIV and
                               Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia; attention deficit disorder; anxiety; depression; bipolar disorder; neurological disorder; Huntington's disease; dementia; obesity; anorexia; metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer; cardiomyopathy; atheroscalerosis; human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser; antidepressant; anorectic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity -
Protein-Coupled Receptor (GPCR) polypeptide #35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 35; Page 83; 279pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vogeli G, Wood LS, Parodi LA,
                                                                                                                                                                                                                                                                                                                                                               23-FEB-2000; 2000US-0184247.
23-FEB-2000; 2000US-0184303.
23-FEB-2000; 2000US-0184305.
23-FEB-2000; 2000US-0184305.
23-FEB-2000; 2000US-0184305.
23-FEB-2000; 2000US-01864397.
03-MAR-2000; 2000US-018680.
03-MAR-2000; 2000US-018880.
03-MAR-2000; 2000US-018880.
13-WAR-2000; 2000US-013861.
11-UUL-2000; 2000US-0213861.
11-UUL-2000; 2000US-0213861.
11-UUL-2000; 2000US-0213861.
11-UUL-2000; 2000US-0213861.
20-UUL-2000; 2000US-0213861.
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N-PSDB; AAS42840.
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  Human
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CC AAY90677 and AAA30709-A30743 and AAA30779-A30779). The mutant proteins of the invention Contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-pro. The endogenous amino acid is selected from Lys, His, Arg or AA,15-pro. The endogenous amino acid is selectably the endogenous is preferably tye. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably the ready of stretch between the substituted amino acid and the Proc TM is a mino acid stretch between the substituted amino acid and the Proc TM is be endogenous. An endogenous and con-endogenous residues. The constitutively acive GPCRs are useful for identifying antagonists, agonists and partial agonists for use as constitutional agents. The mutant proteins are also useful in research setting diseases and disorders associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous considers. Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; mutant; mutein. Human mutant G protein-coupled receptor GPR17 (V234K). Example 2; Page 233-234; 341pp; English. Behan DP, Chalmers DT, Liaw CW human GPCRs of the invention 99WO-US23938. (first entry) (AREN-) ARENA PHARM INC. WPI; 2000-329165/28. N-PSDB; AAA30718. Ą, WO200022129-A1. 12-OCT-1999; 13-OCT-1998; 21-AUG-2000 20-APR-2000. Homo sapiens Synthetic. Sequence

101 GLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLL 160

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Query Match
22.2%; Score 417; DB 22; Length 177;
Best Local Similarity 58.9%; Pred. No. 4.3e-36;
Matches 93; Conservative 8; Mismatches 17; Indels 40; Gaps

177 AA;

Sequence

14 GVCALHRHL-----RGVYLMACVSVDHYPAVVCAHWGPCLRTAGRARLVCVAIWTLVLL

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RESULT 12
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                                                                            97 WPFGEIACRLTGFLFYLMMYASIYFLTCISADRFLAIVHPVKSLKLRRPLYAHLACAFLW 156
                                                                                                    214
                                                                                                                  157 VVVAVAMAPLLVSPQTVQTMHTVVCLQLYREKAS----HHALVSLAVAFTFPFITTVTC 211
                                                                                                                                    YMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFMARGMLHL 274
                                                                                                                                                                   275 PSCAERRAFLLISLQATVALMNNNCGITPIIYFFASTHYRKWLLGIL---KLKG---SSSS 328
                                                                                                                                                                              267 ASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEG 326
                                                                  96 WPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIW 155
                                                 96
                                             FYLLDFILALVGNTLALWERTRDHKSGTPANVFLWHLAVADLSCVLVLPTRLVYHFSGNH
                                                                                                                                               TLVLLQTMPLLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGFCGPVGIILSC
                                  36 FYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSS
                  Gaps
21.1%; Score 395.5; DB 21; Length 339; 30.5%; Pred. No. 2e-33; ive 57; Mismatches 142; Indels 17;
                                                                                                                                                                                                                                                                                                                                        Primer; seven transmembrane receptor; receptor; amplification.
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/label≈ Transmembrane domain.
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/label= Transmembrane domain.
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/label= Transmembrane
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                                                                                                                                                                                                                                                                                                                         Seven transmembrane receptor (R12).
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(first entry)
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/label= Tr
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                  95; Conservative
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                                                                                                                                                                                                      SSSSSSTPGKA 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-200264/24.
Query Match
Best Local Similarity
Matches 95; Conserv
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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07-PEB-1995
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                                                                                                    156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 WPPGEIACRLIGFLFYLNMYASIYFLTCISADRFLAIVHPVKSLKLRRPLYAHLACAFLW 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 VVVAVAMAPLIVSPQTVQTNHTVVCLQLYREKAS----HHALVSLAVAFTFPFITTVTC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 YMXITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCPSPYHLNIKQFMARGMLHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 PSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWLLGIL---KLKG---SSSS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 ASCATORILALANRITSCLTSINGALDPIMYFEVAEKFRHALCNLLCGKRLKGPPPFFEG 326
                                                                                                                                                                                pCR using two primers (AAO66174, AAO66175) was performed to amplify a partial sequence of the R20 seven transmembrane coding sequence which was later used as a probe for isolating the R20 genomic clone (AAO66176) from a human placenta DNA library. During the Isolation of the R20 gene, two weakly hybridising sequences were identified which had significant homology to other seven transmembrane receptors. The probe was used to screen a human genomic foetal liver DNA library, and while the R20 gene could not be identified in this library, several weakly hybridising clones were plaque purified, subcloned and sequenced. The two clones were designated (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 PYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 TLVLLQTMPLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGFCGPVGIILSC
DNA encoding seven trans:membrane receptors - used to develop prods. for use as therapeutic or diagnostic agents for conditions involving the receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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antagonist; haemophilia; wound healing; restenosis; angina;
inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 20.9%; Score 391.5; DB 15; Length Local Similarity 30.5%; Pred. No. 5.4e-33; les 95; Conservative 57; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G-protein thrombin-like receptor.
                                                                                                                               English.
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                                                                                                                               Example 10; Page 81-82; 100pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 KTNESSLSAKS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AA,
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93US-0153848
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Matches 95; Conservative
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N-PSDB; AAV18356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 ASCATORILALANRITSCLTSINGALDPIMYFFVAEKFRHALCNILCGKRLKGPPPSFEG 326
                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
immunology; inflammation; R12.
                                                                                                                                                                  A novel human 7-transmembrane receptor (AAW07617) has been putatively identified as a G-protein thrombin receptor. Its amino acid sequence was deduced from a cDNA clone (AAT4402) discovered in a human infant brain cDNA library. Recombinant receptor can be produced in host cells (e.g. E. coli, COS-7, Sf9) and used to raise antibodies or to screen for (antipagonist cpda. Agonists can be used to treat e.g. haemophilia or to promote wound healing; antagonists can be used to treat inflammation, angina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSS
                                                                                                                                                                                                                                                                                                                                                       TLVLLQTMPLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGPCGPVGIILSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFMARGMLHL
                                                                                                      Human G-protein thrombin receptor, HIBEB69 - useful to identify (ant) agonists, for treatment of angina, restenosis, wound healing
                                                                                                                                                                                                                                                                                              ch 20.9%; Score 391.5; DB 18; Length 339; Similarity 30.5%; Pred. No. 5.4e-33; 95; Conservative 57; Mismatches 142; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human R12 seven transmembrane (7TM) receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 339 AA.
                                                                                                                                                Claim 1, Fig 1A-D; 58pp; English
                              (HUMA-) HUMAN GENOME SCI INC.
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                                                                         WPI; 1997-043073/04.
                                                  Li Y,
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Best Local Similarity
                                                                                                                                                                                                                                                                            Sequence 339 AA;
                                                                                  N-PSDB; AAT44092
           06-JUN-1995;
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                                                   Socayne JD,
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212 YLLIIRSLRQGLRVE----KRLKTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the human R12 protein which is encoded by the full length genomic R12 clone (AAV18356) which was isolated from a human genomic fetal liver DNA library. The invention claims for the full length V28 genomic DNA sequence (AAV18343) isolated from a human placenta genomic library. The V28 (AAW48722) and R12 proteins are seven transmembrane (T7M) receptors which are probably involved in signal by an an be used to produce the recombinant polypeptide, to produce antiev28 antibodies or in screening assays for V28 agonists or antagonists. The antibodies, agonists and antagonists could then be used to modulate V28 receptor-ligand binding, for e.g. in immunological and/or inflammatory events in vivo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding V28 seven transmembrane receptor polypeptide - useful for producing recombinant polypeptide and anti-V28 antibodies, and in screening assays for V28 agonists and antagonists
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'note= "Transmembrane domain 1"
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/note= "Transmembrane domain 3"
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290..312
/note= "Transmembrane domain 7"
                                                                                                                                                                                           "Transmembrane domain 4"
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/note= "Transmembrane domain
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267 ASCATORILALANRITSCLTSINGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEG 326
   PSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWLLGIL---KLKG---SSSS
                                                                                                                                                                                                        G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening;
agonist; antagonist.
                                                                                                                                                                                       Human G protein-coupled receptor GPR17,
                                                                                                                        AAY90618 standard; Protein; 339 AA.
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                                                329 SSSSSSTPGKA 339
                                                              327 KTNESSLSAKS 337
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                                                                                                                                                                                                                                                                                                                                                             (AREN-) ARENA PHARM INC.
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ID AAY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFWARGMLHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 TLVLLQTMPLLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGFCGPVGIILSC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 VVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKAS-----HHALVSLAVAFTFPFFITTVTC 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a novel seven transmembrane (7TM) receptors (also known as heptahelical, serpentine or G-protein-coupled receptors). The coding sequence for the present sequence may be used for gene therapy for diseases such as cancer.
267 ASCATORILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymucleotide encoding seven transmembrane receptors, antibody specific to the receptor, agonist and antagonist of the receptor useful for treating inflammation in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 FYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                              Seven transmembrane receptor; 7TM; heptahelical; serpentine; G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.9%; Score 391.5; DB 21; Length llarity 30.5%; Pred. No. 5.4e-33; Conservative 57; Mismatches 142; Indels
                                                                                                                                                           Human 7TM receptor R12 cDNA clone protein.
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                                                                                               AAB21697 standard; Protein; 339 AA.
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98US-0088337.
92US-0977452.
93US-0153848.
                                                                                                                                                                                                                                                                                          99US-0299843
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                       329 SSSSSSTPGKA 339
                                            327 KTNESSLSAKS 337
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Matches 95, Conserva
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N-PSDB; AAA91725.
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CC AAY90677 and AAA9079), and to DNA encoding them (AAA3079-A30779) and transmembrane domain 6 (The invention contain a materion in a portion of the protein comprising intracellular loop 3 (1C3) and transmembrane domain 6 (TMG). A non-endogenous amino acid, X, is substituted for an endogenous proline in TMG to form a sequence of soids N-terminal of an endogenous proline in TMG to form a sequence of the substituted form and sequence of acids N-terminal of an endogenous maino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this or Ala, and is preferably Lys. When the substituted amino acid and the Process of the acid and an endogenous, non-endogenous, or a mixture of endogenous and may be endogenous, non-endogenous, or a mixture of endogenous and connendogenous residues. The constitutively active of endogenous and partial agonists for use as pharmaceutical agents. The mutant proceins are also useful for settings for elucidating the roles of the receptors in normal and streating diseases and disorders associated with that receptor. Because the endogenous and disorders associated with that receptor. Because the endogenous and disorders associated with the constitutively active, they can be useful for the present sequence represents a human wild-type GPCR referred to in an exemplification of the invention.
Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                             Example 1; Page 126-127; 341pp; English.
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96 WPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIW 155
                                                                                                                                                                                    156 TLVLLQTMPLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVARAIGFCGPVGIILSC 214
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                                                                                                                                                                                                                                                                                                                          215 YMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCPSPYHLNIKQFWARGMLHL 274
                                                                                                                                                                                                                                                                                                                                                    275 PSCAERRAFILISLQATVALMNWNCGITPIIYFFASTHYRKWLLGIL---KLKG---SSSS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                    267 ASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEG 326
                                                                              36 FYTALLUVFSALGNILALCITCQKSRKINCTGIYLVHLAVSDLLFTVALPGRUVCYVLGSS 95
                                                                                                          Query Match 20.9%; Score 391.5; DB 21; Length 339;
Best Local Similarity 30.5%; Pred. No. 5.4e-33;
Matches 95; Conservative 57; Mismatches 142; Indels 17; Gaps
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62 INCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLM
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US-08-383-750-4
; Sequence 4, Application US/08383750
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1 MIKLGPYFTPPTKIKTKIKD.....SETPSITQARGSMFLAEHVV
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.: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
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.: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata1/iaa/BECOMB.pep:*
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Compugen Ltd.
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US-08-383-750-4
US-08-352-678-4
US-09-170-496D-78
PCT-US93-09636-4
US-09-170-496D-182
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US-08-1812-871-3
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US-08-485-886-220
US-08-477-362-220
US-08-477-134-220
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 GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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38.5%; Pred. No. 3.6e-39;
iive 69; Mismatches 139; Indels
     US-08-911-320A-3

US-08-742-440A-7

US-08-742-440A-7

US-08-473-489A-57

US-08-473-489A-220

US-08-474-410-7

US-08-485-695-220

US-08-101-101-3

US-08-101-101-3

US-08-513-974B-56

US-08-513-974B-56

US-08-513-974B-56

US-08-459-046-2

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Best Local Similarity 38.55
Matches 132; Conservative
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TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Wolf, Greenfield & Sacke, P.C.

600 Atlantic Avenue

Boston

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61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
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GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kief, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Pox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION JATA:
APPLICATION NUMBER: US/08/383,750
                                                                                                                                                                         STREET: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W., STREET: Suite 600
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CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel, L.
REGISTRATION NUMBER: 0627
REFRENCE/DOCKET NUMBER: 0627
TELEFOWN: (202) 371-2500
TELEFAK: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 anino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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; Sequence 4, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
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Best Local Similarity 37.84
Matches 135; Conservative
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
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33.7%; Score 632.5; DB 3; Length 3
Best Local Similarity 37.8%; Pred. No. 6.2e-39;
Matches 135; Conservative 74; Mismatches 141; Indels
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| Patent No. 6500926
| GENERAL INFORMATION:
| APPLICANT: Birkenbach, Mark
| APPLICANT: Kieff, Bliott
| APPLICANT: Kieff, Bliott
| TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
                                                                                                            MEDIUM TITE: TIPPY GIBE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFTANION DATA:
APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATFORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
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REGISTRATION NUMBER: 31,616
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                 Floppy disk
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amino acid
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                                                              COMPUTER READABLE FORM:
   USA
                                                                                                 MEDIUM TYPE:
                           02210
COUNTRY:
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61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
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                                                                                                                                                                                                                                                   Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Birkenbach, Mark
APPLICANT: Kleff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
OCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                   33.7%; Score 632.5; DB 4; 37.8%; Pred. No. 6.2e-39; tive 74; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREE: Sterne, Kessler, Goldstein & Fox STREE: 1100 New York Avenue N.W., Suite 600 STATE: D.C. COUNTRY: U.S.
TITLE OF INVENTION: Receptors
FILE REFRENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUCTIONAL DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 361 amino acids
amino acid
                                                                                                                                                                                                                                                     33.74

Query Match
Best Local Similarity 37.84
Matches 135; Conservative
                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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PCT-US93-09636-4
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Sequence 78, Application US/09170496D
Batent No. 6555339
Batent No. 6555339
BAPPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Mismatches 141;
                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.7%; Score 632.5; DB 4 Similarity 37.8%; Pred. No. 6.2e-39;
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B0801/7044
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,954
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/352,678
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/POCKET NUMBER: B080
TELECOMMUNICATION INFORMATION:
TELEPHONE:: 617-220-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.8
Matches 135; Conservative
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                                                                                              Boston
                                                                                                                                        USA
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US-09-170-496D-78
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                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                    STATE: M. COUNTRY:
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95; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                           US-09-170-496D-182
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US-08-153-848-44
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Best Local
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APPLICANT: Behan, Dominic P.
APPLICANT: Châlmers, Derek T.
APPLICANT: Châlmers, Derek T.
APPLICANT: Châlmers, Derek T.
APPLICANT: Châlmers, Derek T.
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APPLICANT: Châlmers, Derek T.
APPLICANT: Châlmers, Derek T.
APPLICANT: APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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                                                                                                                                           2 IKLGPYFTPPTKI-KTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR 60
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Best Local Similarity 37.8%; Pred. No. 8.6e-39;
Matches 135; Conservative 74; Mismatches 141; Indels 7; Gaps
                                                                                 Gaps
                                                                               7;
                                       33.7%; Score 632.5; DB 5; Length 361; 37.8%; Pred. No. 6.2e-39;
                                                      37.8%; Pred. No. 6.2e->>/
                                                                             Matches 135; Conservative
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US-09-170-496D-206
                                                            Similarity
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US-09-170-496D-206
    PCT-US93-09636-4
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LENGTH: 361
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                                         Query Match
Best Local (
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Sequence 182, Application US/09170496D

Patent No. 655539

Patent No. 655539

Patent No. 655539

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

CURRENT APPLICATION NUMBER: US/09/170,496D

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SOFUL NO 182

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                                                                                 302 CMDPFIYFPACKGYKRKVMRMLKRQVSVSISSAVKSAPEENSREMTET@MIHSKSS 358
299 GITPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSSTPGKAS---SETPSITQARGS 352
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Sequence 44, Application US/08153848
Patent No. 5759804
GENERAL INPORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Schwelkart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & ADDRESSEE: Bichnell
STREET: 6310 Sears Tower, 233 South Wacker Drive
CITY: Chicago
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3174 Porter Dr
                        Palo Alto
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LIBRARY: General
1992700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.9%; Score 391.5; DB 1; Length 339; Best Local Similarity 30.5%; Pred. No. 2.1e-21; Matches 95; Conservative 57; Mismatches 142; Indels 17
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Sequence 3, Application US/08812871

Patent No. 5955303

Patent No. 5955303

PAPLICANT: Au-Young, Janice

APPLICANT: Muzong Cheng

TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PEN PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/77,452
FILING DATE: 17-NOV-1992
ATPORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31,344
TELEFHONE: (312) 474-6300
TELEFRAM: (312) 474-6300
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Illinois
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96 WPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVALW 155
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Sequence 44, Application US/09299843A

Patent No. 610475

GENERAL INPORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Godiska, Rushick W.

APPLICANT: Schwelkart, Vicki L.

APPLICANT: Schwelkart, Vicki L.

TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
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20.9%; Score 391.5; DB 2; Length 3
Best Local Similarity 30.5%; Pred. No. 2.1e-21;
Matches 95; Conservative 57; Mismatches 142; Indels
                                                                                                                  MEDIUM TYPE: Discette
COMPUTER: IBM Comparible
OPERATING SYSTEM; DOS
SOFTWARE: FastEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP-0237 US
REPERSNCE/DOCKET NUMBER: PF-0237 US
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0237 US
TELEPHONE: 416-85-055
INFORMATION: TELEPHONE: 416-85-055
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTRISTICS:
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amino acid
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ZIP: 94304
COMPUTER READABLE FORM
MEDIUM TYPE: Disket
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Sequence 44, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION: GALERAL RODAL APPLICANT: GOdiska, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (112) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
US-09-088-337B-44
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                CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STREE: 1111nois
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UW-1998
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
ATTORNEY AGENT INFORMATION:
NAME: Jill E. Uhl
RECLSTAMTION NUMBER: 43,213
RECTRATION NUMBER: 43,213
RECTRATION NUMBER: 43,213
RETRENGE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1970-4448
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
US-09-299-843A-44
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Best Local Similarity
Matches 95; Conserv
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RESULT

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97 WPPGEIACRLTGFLFYLNWYASIYFLTCISADRFLAIVHPVXSLKLRRPLYAHLACAFLW 156
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Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 339;
                                                                                                                                                                                                          STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.9%; Score 391.5; DB 4; Best Local Similarity 30.5%; Pred. No. 2.1e-21; Matches 95; Conservative 57; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Un-1998
CLASSIFICATION: duhrnown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 SSSSSSTPGKA 339
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212 YLLIIRSLRQGLRVE----KRLKTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHG 266
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APPLICANT: LI, YI.

APPLICANT: GOCANNE, JEANINE D
APPLICANT: RUBEN, STEVEN M

ITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS
ADDRESSEE: GRREILA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                 OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT 'APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATONINEY/AGENT INFORMATION:
NAME: NOLANG, Greta B.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 2.1e-21; 57; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.9%; Score 391.5; Best Local Similarity 30.5%; Pred. No. 2.1
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31794
TELECOMONICATION: INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Conservative
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COMPUTER READABLE FORM:
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STATE:
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GRUERAL INC. 033333
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE OF INVENTION: Receptors
FILE REFERENCE: AREN 0040
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 ASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPFSFEG 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.9%; Score 391.5; DB 4; Length 30.5%; Pred. No. 2.1e-21; rive 57; Mismatches 142; Indels
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
IITLE OF INTENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TT-US93-11153-44
Sequence 44, Application PC/TUS9311153
GENERAL INFORMATION:
                                                                                                                     US-09-170-496D-32; Sequence 32, Application US/09170496D; Patent No. 6555339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95; Conservative
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327 KTNESSLSAKS 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; CRGANISM: Homo sapiens
US-09-170-496D-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 95; Conserv
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 32
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96 WPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIW 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.9%; Score 391.5; DB 5; Length 339;
30.5%; Pred. No. 2.1e-21;
ive 57; Mismatches 142; Indels 17; Gaps
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 201-994-1704
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: A39 amino acide
TYPE: amino acid
TYPE: TYPE: protein
PCT-US95-07180-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.9%
Best Local Similarity 30.5%
Matches 95; Conservative
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Search completed: February 19, 2004, 19:35:29 Job time : 22 secs

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February 19, 2004, 19:33:05; Search time 40 Seconds (without alignments) 1884.441 Million cell updates/sec
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1876
1 MIKLGPYFTPPTKIKTKIKD......SETPSITQARGSMFLAEHVV 360
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2: /cgn2 6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2 6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2 6/prodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2 6/prodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2 6/prodata/1/pubpaa/USO7_NEW_PUB.pep:*

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8: /cgn2 6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2 6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801455 seqs, 209382283 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protéin search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 34, Appl	Sequence 1620, Ap	Sequence 1294, Ap	Sequence 109, App	Sequence 17, Appl	Sequence 110, App	Sequence 2, Appli	Sequence 78, Appl	Sequence 112, App	Sequence 206, App	Sequence 95, Appl	Sequence 182, App	Sequence 12, Appl	Sequence 2, Appli	Sequence 4, Appli
SUMMARIES	US-10-041-615-34	US-10-017-161-1620	: US-10-292-798-1294	US-10-041-615-109	US-09-827-937A-17	US-10-041-615-110	US-10-222-024-2	US-10-251-385-78	US-10-225-567A-112	US-10-251-385-206	US-09-791-932-95	US-10-251-385-182	US-09-848-889-12	US-09-788-133-2	US-09-828-478-4
90	12	15	12	12	σ	12	12	15	15	15	11	15	Ω,	σ	10
% Query Match Length DB	360	323	323	229	348	361	361	361	361	361	177	339	339	339	339
% Query Match	100.0	47.1	47.1	38.4	33.9	33.7	33.7	33.7	33.7	33.6	22.2	21.1	20.9	20.9	20.9
Score	1876	884	884	721	635.5	632.5	632.5	632.5	632.5	630.5	417	395.5	391.5	391.5	391.5
Result No.		N	m	4	ហ	9	7	80	σ	10	11	12	13	14	15

Sequence 4, Appli Sequence 1, Appli Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 112, Appl	30 1111 1111 255 1	
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-1.13k	DB 12; 3e-164; 0;	FYTA FYTA	WPFG
3PCR	Score 1876; DB 12; Pred. No. 3.3e-164; Mismatches 0;	RST.	GSS
115	876. 10.	KIPI KIPI	CYV
ULT 1 10-041-615-34 equence 34, Application US/10041615 equence 34, Application US/10041615 ublication No. US20040014038A1 REKERAL INFORMATION: APPLICANT: Edaman, State J APPLICANT: Edinger, Shlomit R APPLICANT: Elieman, Karen APPLICANT: Bileman, Karen APPLICANT: Padigaru, Muralidhara APPLICANT: Rekuda, Ramesh APPLICANT: Padigaru, Muralidhara RITLE OF INVENTION: NO. US20040014038A1e1 FILE REFERENCE: 21402-233-061 CURRENT FILING DATE: 2003-01-29 PRIOR APPLICATION NUMBER: 60/259,552 PRIOR APPLICATION NUMBER: 60/259,552 PRIOR APPLICATION NUMBER: 60/269,544 PRIOR FILING DATE: 2001-01-03 PRIOR FILING DATE: 2001-01-03 PRIOR FILING DATE: 2001-01-03 PRIOR FILING DATE: 2001-01-03 PRIOR FILING DATE: 2001-01-03 NUMBER OF SEQ ID NOS: 174 ILENGTH: 360 ILENGTH: 360 ITYPE: PRI TYPE: PRI TYPE: PRI TYPE: THE TENDER TO SAPIENCE TO COLL SAPIENCE TO CO	re l d. N	SOTA SOTA	GRW
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-34 'Application US/100416 'ADDLICATION US/2004014038A1 'ORMATION: Casman, Stacie J Edinger, Shlomit R Ellerman, Karen Smithson, Glennda Kekuda, Ramesh Padigaru, Muralidhara NUVENTION: NO. US2004001. ENCE: 21402-233-061 ENCE: 21402-233-061 ENCE: 21402-233-061 ENCE: 21402-233-061 ENCE: 21402-233-061 ENCE: 21402-233-061 ENCE: 21402-233-061 ENCE: 2001-01-03 ICATION NUMBER: 60/259, NG DATE: 2001-01-03 ICATION NUMBER: 60/260, NG DATE: 2001-01-03 ICATION NUMBER: 60/277, NG DATE: 2001-01-03 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-04 ENCE ID NOS: 174 FOMO SAPPIER: 2001-01-04 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-01-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-03-20 FOM SAPPIER: 2001-03-20 ENC ID NOS: 174 FOMO SAPPIER: 2001-03-20 FOM SAP	ilar Cor	KLG KLG KLG	NCTO
-615-34 -615-34 tion No. US20040014038A INFORMATION: ANT: Casman Stace J ANT: Edinger, Shlomit ANT: Edinger, Shlomit ANT: Edinger, Shlomit ANT: Smithson, Glennda ANT: Smithson, Glennda ANT: Feright Nuralid CONTINUENTION: AND SAGISTON NUMBER: TAPPLICATION NUMBER: 00/APPLICATION NUMBER: FILING DATE: 2001-01-09 APPLICATION NUMBER: 60/ FILING DATE: 2001-01-09 FILING DATE: 2001-01-09 FILING DATE: 2001-01-09 FILING DATE: 2001-01-09 FILING DATE: 2001-01-03 FILING DATE: 2001-03-20 OF SEQ ID NOS: 174 H: 360 PRIL NOS: 174 H: 360 PRIL HOMO SADISH NOS: 174 FILING DATE: AND SET NOS: 174 FILING DATE: AND SET NOS: 174 FILING DATE: AND SET NOS: 174 FILING DATE: AND SET NOS: 174 FILING DATE: AND SET NOS: 174 H: 360	tch al Sim 360;	1 H	1 KI
RESULT 1 US-10-041-615-34 Sequence 34, Application US/10041 Sequence 34, Application US/10041 GENERAL INFORMATION: APPLICANT: Edinger, Shlomit R APPLICANT: Edinger, Shlomit R APPLICANT: Edinger, Shlomit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: Smithson, Glannit R APPLICANT: No. US20400 FILE REFERENCE: 21402-233-061 CURRENT FILING DATE: 2001-01-03 PRIOR FILING			9
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APPLICANT: ASA1, KIYOSHI
APPLICANT: ASA1, KIYOSHI
APPLICANT: ASA1, KIYOSHI
APPLICANT: ASATAN, VUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REPERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
PRIOR PILING DATE: 2001-12-18
PRIOR PLING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENTION NUMBER: J. 2011-06-18
SOFTWARE: PATENTION NOS: 2010
SOFTWARE: PATENTION NOS: 2010
SEQ ID NOS: 2010
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301 TPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSTPGKASSETPSITQARGSWFLABHVV 360
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                                                                             MACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLAC 180
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                            61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
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58; Gaps
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Sublication No. US20030143668A1

Sublication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUMA, WARKINO

APPLICANT: ASTAI, KIYOSHI

TITLE OF INVENTION: NOVEL OF PROTEIN-COUPLED RECEPTORS

TITLE OF INVENTION: NOVEL OF PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/012

CURRENT FILING DATE: 2002-12-18

FRICA FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE PARENCE: 085 10 NOS: 2430

SOFTWARE PARENCE: 2002-66-18

LENOTAL 323

LENOTAL 323
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Matches 195; Conserva
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APPLICANT: Casman, Stacie J
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APPLICANT: Bdinger, Shlomt R
APPLICANT: Blinger, Shlomt R
APPLICANT: Blinger, Shlomt R
APPLICANT: Blinger, Shlomt R
APPLICANT: Brithson, Glennda
APPLICANT: Rekuda, Ramesh
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: 0. US20040014038Alel GPCR-Like Proteins and Nucleic Acids Encodi
FILE REPERENCE: 21402-233-061
CURRENT FILING DATE: 2003-01-29
FRIOR APPLICATION NUMBER: 60/259,552
FRIOR APPLICATION NUMBER: 60/260,544
FRIOR APPLICATION NUMBER: 60/260,544
FRIOR APPLICATION NUMBER: 60/277,405
FRIOR FILING DATE: 2001-01-09
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65.7%; Pred. No. 4.7e-73;
tive 8; Mismatches 36; Indels 58; Gaps
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                                                                                                                                                                                                                                                                   Best Local Similarity 65.7%
Matches 195, Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1294
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US-10-041-615-109
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LENGIH: 229
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; Sequence 1294, Application US/10292798 ; Publication No. US20030235833A1 ; GENERAL INFORMATION:

US-10-292-798-1294

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240 INTIILIIVVFVLCFTPYHVAIIQHMIXKLRFSNFLECSQRHSFQISLHFTVCLMNFNCC 299
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                                                                                                                                                                                                                118 YLWACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTWPLLLMPMTKPLVGKL 177
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                                                                                       59 SRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGV
                                                                                                              66 SRKINCTGIYLVHLAVSDLLFTVALPGRVLAFRQGALQ--ADGVCALHRHL-----RGV
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Length 229;
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33.9%; Score 635.5; DB 9; Length
Best Local Similarity 38.5%; Pred. No. 3.6e-50;
Matches 132; Conservative 69; Mismatches 139; Indels
  Score 721; DB 12; Length 2:
Pred. No. 3e-58;
5; Mismatches 12; Indels
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Sequence 17, Application US/09827937A
Sequence 17, Application US/09827937A
Sequence 17, Application US/09827937A
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Huben, Steven M.
TITLE OF INVENTION: Human G-Protein Coupled Receptors;
TITLE OF INVENTION: Human G-Protein Coupled Receptors;
CURRENT APPLICATION UNMERS: US/09/827,937A
CURRENT FILING DATE: 2001-04-09;
PRIOR FILING DATE: 1997-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 348
                                           5; Mismatches
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US-10-041-615-110
S-10-040-615-110
; Sequence 110, Application US/10041615
; Publication No. US20040014038A1
; GENERAL INFORMATION:
    Query Match
Best Local Similarity 85.1%;
Matches 143; Conservative
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; ORGANISM: Homo sapiens
US-09-827-937A-17
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APPLICANT: Smithson, dilenma.
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Fadigaru, Muralidhara
TITLE OF INVENTION: US20040014038Alel GPCR-Like Proteins and Nucleic Acids Encod
FILE REFERENCE: 21402-233-061
CURRENT APPLICATION NUMBER: 60/259,552
PRIOR APPLICATION NUMBER: 60/259,552
PRIOR APPLICATION NUMBER: 60/260,544
PRIOR APPLICATION NUMBER: 60/277,405
PRIOR APPLICATION NUMBER: 60/277,405
PRIOR APPLICATION NUMBER: 60/277,405
NUMBER OF SEQ ID NOS: 174
SOPTWARE: CuraSeqList version 0.1
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Publication No. US20030104487A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pfizer Ltd. (GB)
APPLICANT: Pfizer Ltd. (GB)
APPLICANT: Pfizer Ltd. (GB)
TITLE OF INVENTION: Neuropeptide receptor and uses thereof
FILE REPERENCE: PCS22032
CURRENT APPLICATION NUMBER: US/10/222,024
CURRENT PILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-08-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 361
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Matches 135; Conservative
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US-10-222-024-2
                                                                                                                                                                                                                                                                                                                                                                                             : Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo
US-10-041-615-110
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LENGTH: 361
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Best Local
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Sequence 112, Application US/10225567A

Sequence 112, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: InfeSpan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TILLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 1220-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: Patentin version 3.1

SEQ ID NO 112

LENGHAL 361

TURNEL DATE: 2000-12-19

SEQ ID NO 112

LENGHAL 361
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US-200-251-385-206

Publication No. US20030105292A1

Publication No. US20030105292A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Protein-Coupled

TITLE OF INVENTION: Protein-Coupled

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors
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                                                299 GITPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSSTPGKAS---SETPSITQARGS 352
                                                                                                                                                  299 GITPIIYFFASTHYRKWLLGILKLKGSSSSSSSSSTPGKAS---SETPSITQARGS 352
                                                                                                                                                                                               302 CMDPFIYFFACKGYKRKVWRMLKRQVSVSISSAVXSAPEENSREMTETQMMIHSKSS 358
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ORGANISM: Homo sapiens
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Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Dehan, Dominic P.
APPLICANT: Liaw, Chen W.
ITLE OF INVENTION: Protein-Coupled
ITLE OF INVENTION: Protein-Coupled
ITLE OF INVENTION: Protein-Coupled
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ITLE OF INVENTION: Protein-Coupled
ITLE OF INVENTION NUMBER: US/10/251,385
INVENTION OF SEQ ID NOS: 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
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    Length 361;
ch 33.7%; Score 632.5; DB 15; Length I Similarity 37.8%; Pred. No. 7.1e-50; Conservative 74; Mismatches 141; Indels
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Matches 135;
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Sequence 182, Application US/10251385

Publication No. U520030105292A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

ITLE OF INVENTION: Protein-Coupled

ITLE OF INVENTION: Receptors

ITLE OF INVENTION: Receptors

ITLE OF INVENTION: Receptors

ITLE OF INVENTION: Receptors

ITLE OF INVENTION: Receptors

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ITLE OF INVENTION: Receptors

ITLE OF INVENTION: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SOFTWARE: PatentIn version 3.1

SEQ ID NO 182

ILENGER: PatentIn version 3.1
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Pred. No. 2e-30;
8; Mismatches
                PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-09
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PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-07-14
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60/217,370
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il Similarity 58.9%;
93; Conservative
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Best Local Similarity 30.5*
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CRGANISM: Homo sapiens
US-10-251-385-182
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US-09-791-932-95
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APPLICANT: Parodi, Luis A.
APPLICANT: Parodi, Luis A.
APPLICANT: Hibber, Ronald R.
APPLICANT: Hibber, Ronald R.
APPLICANT: Hidber, Ronald R.
APPLICANT: Walerie
APPLICANT: Ruff, Valerie
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CURRENT APPLICATION NUMBER: 06/184,305
PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.6%; Score 630.5; DB 15; Length Best Local Similarity 37.8%; Pred. No. 1.1e-49; Matches 135; Conservative 74; Mismatches 141; Indels
                       CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER: OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
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Publication No. US20030003451A1
GENERAL INFORMATION:
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APPLICATION NUMBER: FILING DATE: 2000
                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-251-385-206
                                                                                                                                                                                                                       SEQ ID NO 206
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WPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIW 155
                                                                                                                                   157 VVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKAS-----HHALVSLAVAFTFPFITTVTC 211
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                              TLVLLQTMPLLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGFCGPVGIILSC
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NAME/KEYS: misc feature

OTHER INFORMATION: Incyte ID No. US20020025555A1 G992700
US-09-848-889-12
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APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
FILE REFERENCE: PC-0042 CIP BABNOSTIC FOR BRAIN CANCER
FILE REFERENCE: PC-0042 CIP CURRENT APPLICANTON NUMBER: US/09/848,889
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
SEQ ID NO 12
LENGTH: 339
TYPE: PRT
GRANISM: Homo sapiens
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Patent No. US20020155528A1

GENERAL INTERNATION:

APPLICANT: Xiao, Yonghong

TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR

TITLE OF INVENTION: Protein

FILE REFERENCE: 04974.00458

CURRENT APPLICATION NUMBER: US/09/828,478

CURRENT APPLICATION NUMBER: 60/195,196

PRIOR PRILING DATE: 2000-04-09

PRIOR FILING DATE: 2000-14-09

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 16

SEQ ID NOS: 16

IENGTH: 339
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                                                   GREAL INCORNATION:
APPLICANT: GLAXO GROUP LTD
TITLE OF INVENTION: ASSAY:
FILE REPERENCE: P79011
CURRENT APPLICATION NUMBER: US/09/788,133
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
                   Sequence 2, Application US/09788133 Patent No. US20020052001A1
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ORGANISM: homo sapiens
-09-788-133-2
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157 UVVANAMAPLLVSPQTVQTNHTVVCLQLYREKAS ----HHALVSLAVELAPFITTVTC 211
215 YMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYTLNIKQFWARGMLHL 274
212 YLLIIRSLRQGLRVE-----KRLKTKAVRMIAIVLAIFLVCFVPYHVNRSVYVLHYRSHG 266

156 TLVLLQTMPLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGFCGPVGIILSC 214

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Oy 329 SSSSSTPGKA 339
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Db 327 KTNESSLSAKS 337
Search completed: February 19, 2004, 19:36:22
Job time : 41 secs
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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 19, 2004, 19:30:15; Search time 20 Seconds (without alignments) 1731.036 Million cell updates/sec Run on:

US-10-041-615-34 1876 1 MIKLGPYFTPPTKIKIKD......SETPSITQARGSMFLAEHVV 360 Title: Perfect score: 1 Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	G protein-coupled	alpha-thrombin rec	thrombin receptor	thrombin receptor	thrombin receptor		G protein-coupled		G protein-coupled	G protein-coupled	ATP receptor P2u -	G protein-coupled	chemokine (C-C) re	interleukin-8 rece	angiotensin recept	probable chemoattr	interferon-inducib	interleukin-8 rece	interleukin-8 rece	G protein-coupled	œ	heptahelical P2Y5-	G protein-coupled	obable G		8	probable G protein	Ъ	interleukin-8 rece
SUMMARIES		O.	B45680	\$17148	A37912	A43448	151667	JC4800	JC5067	A57160	JC5498	155450	A47556	A39714	A45177	A53611	I38435	JC5796	JE0349	A53752	A48921	I50241	JQ1231	JC5549	A30341	S40685	T09508	A54946	S30508	I49341	A39445
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		Score	632.5	364.5	339.5	339	332.5	329	324	322.5	315.5	308	308	307.5	307	306.5	302	300.5	300	298.5	298.5	297.5	297	296	293.5	293	291.5	290.5	290.5	289.5	œ
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chemokine (C-C) re	chemokine (C-C) re	probable G protein	somatostatin recep	delta opioid recep	MIP-1 alpha recept	G protein-coupled	G protein-coupled	adrenomedullin rec	somatostatin recep	P2Y receptor - bov	proteinase-activat	angiotensin II rec	G protein-coupled	mu opioid receptor	הש[תונים-הושלמדת ה
JC4587	G02436	158186	A44021	I38532	I49340	JC4737	B57641	JC5784	JC2083	JC4162	S66518	S44425	S68207	A57510	TESOSS
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ALIGNMENTS

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RESULT 1 B45680 G protein-coupled peptide receptor EBI 2 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Bep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 C;Accession: B45680 R;Birkenbach, M; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E. J, Virol. 67, 2209-2220, 1993 A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled A;Textus: preliminary A;Molecule type: nuclect acid A;Seadules: 1-361 - BIR A;Coss-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057 A;Coss-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057 A;Coss-reference extracted from NCBI backbone (NCBIN:127096, NCBIP:127097) C;Keywords: G protein-coupled receptor; transmembrane protein	Query Match 31.7%; Score 632.5; DB 2; Length 361; Best Local Similarity 37.8%; Pred. No. 5.5e-48; Matches 135; Conservative 74; Mismatches 141; Indels 7; Gaps 4; Qy 2 IKLGPYFPPTKI-KTKIKDLNVESQTVKIFIKSLFYTALLVFSALGNILALCITCQKSR 60	

RESULT 2 S17148 alpha-thrombin receptor - Chinese hamster

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87 PPMPPPPFIS---EDASGYLTSPWITLFIPSV-YTFVFIVSLPLNILAIAVFFRWKVKK 142
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                                                                                                                                                     GRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLM-----VLV 198
                                                                                                                                                                                                       PYHLNIKQFWARGMLHLPSCABRRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWLL 317
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GRVVCYVLGSSWPFGKGLCRLTAFVLYTDTXGGVYLMACVSVDHYPAVVCAHWGPRLRTA 144
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                                                 199 AF-AIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFS
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29.0%; Pred. No. 4.1e-22;
tive 61; Mismatches 153; Indels
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thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
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Best Local Similarity 29.0<sup>†</sup>
Matches 98; Conservative
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C;Species: Homo sapiens (man)
C;Coll (2.Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C;Accession: A37912 D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell (4, 1057-1068, 1991
A;Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic A;Reference number: A37912; MUID:91168254; PMID:1672265
A;Accession: A37912
A;Molecule type: mRNA
A;Residues: 1-425 <VUA>
A;Consor-references: GB:M62424; NID:g339676; PIDN:AAA36743.1; PID:g339677
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S1748
C;Accession: S1748
A;Rasmussen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani
FERS Lett. 288, 133-128, 1991
A;FERS Lett. 288, 133-128, 1991
A;Accession: S1748; MUID:91348247; PMID:1652467
A;Accession: S17148
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A;Cross-reference
A;Map position: E
C;Keywords: G pro
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17

Gaps

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G protein-coupled receptor CKR-L1 - human
N.Alternate names: Chemokine receptor-like protein TER1; GPR-CY6
S.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
A.Title: Molecular Commun. 227, 846-863, 1996
A.Title: Molecular Commun. 227, 846-863, 1996
A.Molecule type: DNA
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A.Molecule type: DNA
A.Molecule type: LNA
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                                                                                                                                                                                                                                                                                                                                                                                                                             70 VHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLFAFVLYTDTYGGVYLMACVSVDHY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 PAVVCAHWGPRLRTAGR--ARLVCVAIWTLVLLQTMPLLLIMPMTKPLVGKLACMEYS--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 --SMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTARED----PVT-SRKGR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 HWRGCLLTLLMLVAVVVCFSPYHLNIKQFMA-RGMLHLPSCAERRAFLLSLQATVALMNM 296
                                                                                                                                                                                                                                                                                         10 PPTKIKTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYL 69
                                                                                                                                                                                                                                                                                                                                                         14 PPTTC------VYRENFKQLLLPPVYSAVLAAGLPLNICVITQICTSRALTRTAVYT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057; Comment: This protein belongs to the family of beta chemokine receptors. Genetics:
       F;241-264/Domain: transmembrane #status predicted <TWM6>
F;283-305/Domain: transmembrane #status predicted <TWM7>
F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                          34;
                                                                                                                                                  Length 328;
                                                                                                                                                  17.5%; Score 329; DB 2; Length 32 28.0%; Pred. No. 2.4e-21; ive 54; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;3c-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Readduss: 1.35 < NAR>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-355 <BON>
A,Residues: 1-355 <BON>
A,Cross-references: EMBL,U45983; NID:g1245056; PID:
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A;Cross-references: GDB:6053733; OMIM:601834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 NSVLDPILFYFTQKKFRR 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 NCGITPIIYFFASTHYRK 314
                                                                                                                                                                                        Similarity 28.0989; Conservative
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Best Local
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51667
R;Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
A;Rierszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
A;Atle: Thrombin receptor's specificity for agonist peptide is determined by its extract
A;Reference number: I51667; MUD:94195429; PMID:8145852
A;Accession: I51667
A;Accession: I51667
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-420 <GER>
A;Cross-references: EMBL:U09632; NID:9495197; PIDN:AAA18498.1; PID:9495198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 HWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 MHSLSWRIMSRAYMACSFIWLISIASTIPLLVTEQTQ----KIPRLDITTCHDVLDLKDL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VLVAFAIGFC-----GPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 XDFYIYYFSSFCLLFFFVPFIITTICYIGIIRSLSSSSIENSC----KKTRALFLAVVV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVAVVVCFSPYHLNIKOFMARGMLHLPSCAERRAFILLSLQATVALMMNVCGITPIIYFFA 308
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A;Accession.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'M',4328 <HAM>
A;Cross-references: EMBL:US2464; NID:g1407632; PIDN:AAB03572.1; PID:g1407633
A;Croenetics:
A;Gene: P2Y6
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C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
C;Accession: JG4800; G02514
Biochem. Biophys. Res. Commun. 222, 303-308, 1996
A;Titla: Cloning, functional expression and tissue distribution of the humar A;Reference number: JG4800; MUID:96222498; PMID:8670200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCOKSRKINCTGIYLVHLAVS
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K-Hammer, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter,
submitted to the EMBL Data Library, March 1996
A; Reference number: H01373
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Score 332.5; DB 2; Length 26.6%; Pred. No. 1.5e-21; ive 74; Mismatches 155; Indels
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A,Residues: 1-328 <COM>
A,Cross-references: EMBL:X97058
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Best Local Similarity 26.6$
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G protein-manual schouse mouse)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Accession: JC5498
R,Methner, A.; Hermey, G.; Schinke, B.; Hermans-Borgmeyer, I.
Biochem. Blophys. Res. Commun. 233, 336-342, 1997
A,Title: A novel G protein-coupled receptor with homology to neuropeptide and ch A,Reference number: JC5498; MUID:97289630; PMID:9144535
A,Contents: Brain
A,Accession: JC5498
A,Molecule type: mRNA
A,References: GB:U79525; NID:q1732346; PIDN:AAB53769.1; PID:g1732347
C; Comment: This protein is involved in the bone metabolism.
C; Superfamily: vertebrate rhodopsin
F;110-187/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                      146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
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                                                                                                                                                                                                                                                                                           GVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTKYSLNSTTWKVLSSLEINILGLVI
                                                                                                                                                                                                                                                                                                                                                                                      259 -NIVLFLETLVELEVLQDCTFERYLDYAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRT
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                                                                                                                                                                                    147 ARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAFAIGFCG
                                                                                                                                                                                                                                                                                                                                                             PVGIILSCYMKI--TWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCF----SPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 ESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVAL
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                                                                                 ELFLPPL-YSLVFVFGLLGNSVVVLVLFKYYRLRSMTDVYLLNLAISDLLFVFSLPFWG-
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  47;
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                                                      KIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSD)
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16.8%; Score 315.5; DB 2;
Best Local Similarity 25.4%; Pred. No. 4.1e-20;
Matches 89; Conservative 67; Mismatches 154;
  131;
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GILKLKGSSSSSSS 331
     58;
     Conservative
     93;
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                                                                                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 IRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGVLQCYSFYNQQT---LKWKIFTNFKWN 203
                                                                                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 ILGILIPFTIFMFCYIKILHQLKRCQNHNKT------KAIRLVLIVVIASLLFWVP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHINIKQFMARGMIHLPSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWL-- 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 AGRARLVCVAIWTLVILOTMPILIAMPMTKPLVGKLACMEYSSMESVLGLPLMVIVAFAIG 203
                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
Accession: A57160
                                                                                                                                                                                                                                                                                                                                                                                                PGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRT
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,Cross-references: GB:X85740; NID:g1370103; PIDN:CAAS9743.1; PID:g971452; Note: source clone K5-5
                                                                                                                                                                                                               Gaps
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A; Statue: preliminary; not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1-360 < POW>
A; Concestreferences: GB:X85740; NTF
C; Genetiff
                                                                                                                                                              Length 355;
                                                                                                                                                              Ouery Match
17.3%; Score 324; DB 2; Length 355
Best Local Similarity 26.4%; Pred. No. 7.1e-21;
Matches 89; Conservative 65; Mismatches 145; Indels
          transmembrane #status predicted <TM3>
transmembrane #status predicted <TM4+
transmembrane #status predicted <TM5+
transmembrane #status predicted <TM6-
transmembrane #status predicted <TM6-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFOKSCSQIFNYLGRQMPRESCEKSSSCQQHSSRSSS 350
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Pred. No. 9.7e-21;
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NyAlternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revis
C;Accession: A57160
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Best Local Similarity
          F;108-129/Domain: t:
F;147-171/Domain: t:
F;200-222/Domain: t:
F;239-260/Domain: t:
F;281-304/Domain: t:
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A;Accession: A39714
A;Accession: A39714
A;Betaus: nucleic acid sequence not shown
A;Actucle type: mRNA
A;Residues: 1-362 <SRE>
A;Cross-references: GB:M64749; NID:G292418; PID:G292419
C;Comment: The authors have revised the name and functional description of this protein
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor RDC1 - human
C;Species: Homo sapiens (man)
C;Accession: A39714
R;Sreedharan, S.P.; Robichon, A.; Peterson, K.E.; Goetzl, E.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4986-4990, 1991
A;Title: Cloning and expression of the human vascactive intestinal peptide receptor.
A;Reference number: A39714; MUID:91271317; PMID:1675791
                                                                                                                                                                                                                                      141 LRTAGRARLVCVAIWTLVLLQTMPLLLMPWTKPLVGKLACMEYSSMESVLGLPLMVLVAF 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 ELVSVVLGFAVPFSIIAVFYFLLARAISASSDQEKHSSRK-----IIFSYVVVFLVC 264
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28 NEDFKYYLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLP 87
                                                                                                                           88 LLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLRNG--
                                                                                                                                                                                                                                                                                             146 --RARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVML
                                                                            GRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVV----CAHWGPR
                                                                                                                                                                                                                                                                                                                                                                                               201 AIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAV-VVCFSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 HLNIKOFMARGMLHLPSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 KPPTEPTPSPQARRKLGLHRPNRTVRKDLSVSSDDSRRTESTP--AGSBTKDI 371
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16.4%; Score 307.5; DB 2; Length 362;
Best Local Similarity 24.2%; Pred. No. 2e-19;
Matches 80; Conservative 74; Mismatches 148; Indels 29
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                                                                                                                       Describes Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Decies: 02-011-1996 #sequence_revision 02-011-1996 #text_change 19-May-2000
C;Accession: 155450
R;Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.
U. Biol. Chem. 270, 26152-26189, 1995
A;Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor. A;Reference number: 155450; MUID:96044682; PMID:7592819
A;Reference number: 155450; MUID:96044682; PMID:7592819
A;Reference number: 155450; MUID:9604682; PMID:7592819
A;Reference number: 155450; MUID:960604682; PMID:7592819
A;Reference number: Conglete from GB/EMBL/DDBJ
A;Residues: 1-328 «RBS)
A;Cross-references: GB:D63665; NID:91066007; PIDN:BAA09816.1; PID:91066008
C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 PPTTC-----VYREDFKRLLLPPVYSVVLVVGLPLNVCVIAQICASRRTLTRSAVYT 65
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A;Molecule type: m2NA
A;Redidues: 1-73 <LUSA
A;Residues: 1-73 <LUSA
A;Coss-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein
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16.4%; Score 308; DB 2; Length 373; 27.2%; Pred. No. 1.9e-19; ative 53; Mismatches 164; Indels

Conservative

Query Match Best Local Similarity Matches 96; Conserv

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nterleukin-8 receptor type B - human
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A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph A;Title: Structure and functional expression of the human macrophage inflammatory 1 alph A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
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   chemokine (C-C) receptor 1 - human
NyAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C; Accession: A55177; I55671
E; Neote, K; DiGregorio, D; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A; Title: Molecular cloning, functional expression, and signaling characteristics of a (A) A; Accession: A45177; MUID: 93161416; PMID: 7679328
A; Etchernce number: A45177; A; Ascession: A45177
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ayap position: 3921-3921

C; Superfamily: vertebrate thodopsin

C; Superfamily: vertebrate thodopsin

C; Superfamily: vertebrate thodopsin

C; Superfamily: vertebrate the status predicted < TMI>
F; Se-60/Domain: transmembrane #status predicted < TMI>
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F; 205-231/Domain: transmembrane #status predicted < TMI>
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F; 205-231/Domain: transmembrane #status predicted < TMI>
F; 240-264/Domain: transmembrane #status predicted < TMI>
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F; 240-264/Domain: transmembrane #status predicted < TMIO-
F; 240-264/Domain: transmembrane #status predicted < TMIO-
F; 240-273, 106-183/Disulfide Doma
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A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
B;Gao, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
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332 SVDRLERVSSTSPST 346
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                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
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A;Cross-references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U11873; 11876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J. B. B. Chem. 269, 11065-11072, 1994 A;Title: Structure, genomic organization, and expression of the human interleukin-8 recells, R;Reference number: A53611; MUID:94209273; PMID:7512557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule_type: DNA,
M.Residues: 6-360 cSPR-
A;Cross-references: GB:M99412; GB:L19593
A;Cross-references: GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253; 1280-1283; 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor A;Reference number: A39446; MUID:91368200; PMID:1891716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:W73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: 137898; 138712; A53611; A39446
R;Ahnja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
B;Ahnja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
A; Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleul
A;Reference number: 137898; MUID:95014476; PMID:7929358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLVAFAIGFCGFVGIILSCY---MKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
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                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-360 (RES)
A;Cross.references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803
A;Accession: 138712
A;Accession: preliminary
A;Gtatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
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Best Local Similarity 28.0%; Pred. No. 2.5e-19;
Matches 94; Conservative 61; Mismatches 144; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 2435-2435
A;Map position: 2435-2435
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 FRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: A39446
A,Status: preliminary, nucleic acid sequence not shown
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angiotensin receptor homolog APJ - human cispecies: Homo sapiens (man)
Cj.Species: Homo sapiens (man)
Cj.Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
Cj.Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
Cj.Date: 15-Mar-1996
Rjo'Dowd, B.P.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr Gene 136, 355-360, 1993
AjTitle: A human gene that shows identity with the gene encoding the angiotensin recepto A, Reference number: 138435; MUID:94124031; PMID:8294032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 VPFTIMLTCYFFIAQTIAGHFRKERI---EGLRKRRRLLSIIVVLVVTFALCMMPYHLVK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 YTALLVFSALGNILALCLTCOKSR-KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Modecule type: DNA
A;Modiques: 1-380 cmss>
A;Cross-references: EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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16.1%; Score 302; DB 2; Length 380;
Best Local Similarity 26.7%; Pred. No. 6.5e-19;
Matches 88; Conservative 67; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 GOSRCAGTSHSSSGEKSASYSSGHSQGPG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 11q12
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: APJ
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Search completed: February 19, 2004, 19:34:56 Job time : 22 Becs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                             OM protein - protein search, using sw model
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Rebruary 19, 2004, 19:18:00 ; Search time 17 Seconds
(without alignments)
995.860 Million cell updates/sec Run on:

US-10-041-615-34 1876 1 MIKLGPYFTPPTKIKTKIKD.....SETPSITQARGSMFLAEHVV 360 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues

Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008.
Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		homo	рошо	crice			P25116 homo sapien		rattus n	P47749 xenopus lae		Q15077 homo sapien			sns	٠.	рошоц	ratt	maca	pod	mue		BUTT	ratt	8118		pan t	homo	homod	P32246 homo sapien	рошо	2 rattı	19 maca	O88410 mus musculu
SUMMERTES	ID	EBI2 HUMAN	GP17 HUMAN	PAR1 CRILO	PAR1 PAPHA	PAR1 MOUSE	PAR1_HUMAN	V206 FOWPV	PAR1_RAT	PAR1_XENLA	P2Y8_XENLA	P2Y6_HUMAN	CKR8 MOUSE	CKR8_HUMAN	CLT1_PIG	CKR4_HUMAN	CLT1_HUMAN	CLT1_RAT	CKR1_MACMU	FK79 HUMAN	CLT1_MOUSE	CML1_HUMAN	CML1_MOUSE	P2Y6_RAT	CLT2_PIG	P2Y2_MOUSE	IL8B_PANTR	1 1	P2Y2 HUMAN	CKR1_HUMAN		P2Y2_RAT	IL8B MACMU	CCR3_MOUSE
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P35414 homo sapien P55919 gorilla gor O35786 rattus norv P49682 homo sapien P35344 oryctolagus P35343 mus musculu Q28003 bos taurus Q99677 homo sapien P3250 gallus gall Q28422 gorilla gor P21109 oryctolagus O97666 macaca mula
APJ HUMAN ILBA GORGO CMLI RAT CCRS HUMAN ILBB RABIT ILBB MOUSE ILBB BOVIN P2YS HUMAN R2YS CHICK ILBB GORGO ILBB GORGO ILBA RABIT APJ MACMU
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ALIGNMENTS

REBULY 14 ID ERIZ HUMAN ENERGY 127, Created) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DT GCCT-1993 (Rel. 27, Last sequence update) DE GRA-1000 (Rel. 27,
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KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
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Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
"A novel orphan G protein-coupled receptor primarily expressed in the novel orphan of promosomal band 2q21.";
J. Neurochem. 70:1357-1365(1998).
-i- FUNCTION: Putative receptor for purines coupled to G-proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                      7.
                                                                                                                                                                                                                                                                                             ; Score 632.5; DB 1; Length 361; Pred, No. 5.3e-38; 74; Mismatches 141; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=96145150; PubMed=8558062;
Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr.,,
Godiska R., Gray P.W.;
"New members of the chemokine receptor gene family.";
J. Leukoc. Biol. 59:18-23(1996).
                                                                                            6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
INTERACTION WITH G PROTEINS.
BY SIMILARITY.
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Q13304; Q9UDZ6; Q9UE21;
Q1-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable P2X purinoceptor GPR17 (P2Y-like receptor) (R12).
                                                                                                                                                                                                                                                  BSA2171F34C9C67B CRC64;
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                              S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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SUBCELLULAR LOCATION: Integral membrane protein.
ALTERANTUE PRODUCTS:
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312
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SEQUENCE
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     TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swigs Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                ISOIG=013304-2; Sequence=VSP 001987; IN BRAIN. TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
Missing (in isoform 2).
/FIIdavsp 001987.
132FBE97BE83C6OC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 603071; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:000186; F:chemokine receptor receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Alternative splicing.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
Event=Alternative splicing; Named isoforms=2;
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                                          me=1;
IsoId=Q13304-1; Sequence=Displayed;
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EMBL; Y12546; CAA73144.1; -.
EMBL; Z94154; CAB08107.1; -.
EMBL; Z94155; CAB08108.1; -.
HSSP; P34996; LDDD.
Genew; HGNC:4471; GPR17.
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275 PSCAERRAFLLSLQATVALMANACGITPIIYFFASTHYRKWLLGIL---KLKG---SSSS 328
                                              295 ASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEG 354
                                                                                                                                                        PARI_CRILO STANDARD; PRT; 428 AA.
Q00991; Q60461;
01-APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                              F2R OR PAR1. Chinese hamster) (Chinese hamster). Stroetulus longicaudatus (Long-tailed hamster). Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                        "CDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca2+ mobilization."; FEBS Lett. 288:123-128(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHOODSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
PROGICE or PROTEIN RECEP_F1_2; 1.
PROGICE OR PROTEIN RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                            MEDLINE=91348247; PubMed=1652467; Raemussen U.B., Youret-Craviari V., Jallat S., Schlesinger Y., Pages G., Pavirani A., Lecocq J.P., Pouyssegur J., Obberghen-Schilling E.;
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REMOVED FOR RECEPTOR ACTIVATION
SIMILARITY).
PROTEINASE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
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                                                                            329 SSSSSSTPGKA 339
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105
131
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106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 YLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTK--PLVG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 KLACMEYSSMESVLGLPLMVLVAF-AIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 GRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFWARGMLHLPSCAERRAFLLSLQATVALMN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 SKKSRALFLSAAVFCVFIVCFGP--TNVLLIMHYLLLSDSPATEKAYFAYLL--CVCVSS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARI PAPHA STANDARD; PRI; 425 AA.
P56488;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 31, Last annotation update)
28-F83-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
P2R CR PARI OR BTHR12.
Papio hamadryas (Hamadryas baboon).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
H-SINKED (GLCNAC. . .) (POTENTIAL).
H-SINKED (GLCNAC. . .)
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: High affinity receptor for activated thrombin coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Score 367; DB 1; Length 428; 30.1%; Pred. No. 3.6e-19; ive 63; Mismatches 158; Indels 1
                                                                                                     4 (FOTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
                             Z (FOIENIIAL).
EXTRACELLULAR (POTENTIAL).
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E5492AB2CD877E2F CRC64;
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ASP/GLU-RICH (ACIDIC).
                                                                 (POTENTIAL).
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(POTENTIAL)
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                                                                                                                                     (POTENTIAL).
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                                                                                                                                                        CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 FKISYYLSGSDWQFGSELCRFVTAAFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLM-----VLV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 AF-AIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 PYHLNIKQPWARGMLHLPSCAERRAFLLSLQATVALMANNCGITPIIYFFASTHYRKWLL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 GRASFICLAIWALAIAGVVPLLLKEQTIQVPG----INITICHDVLNETLLEGYYAYYFS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 AFSAVEFEVPLIISTVCYVSIIRCLSSS----TVANRSKKSRALFLSAAVFCIFIICFG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 SQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G proteins that stimulate phosphoinositide hydrolysis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                     InterPro; ITM, 00276; GPCR_Rhodpsn.
PEAM; PPR0017, 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN RECEP F1 2; 1.
G-procein coupled receptor; Transmem5rane; Glycoprotein; Signal;
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N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
CLEAVAGE (BY THROMBIN).
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EXTRACELLULAR (POTENTIAL)
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HSSP; P34996; 1DDD.
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Matches 101, Conservative
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328 P--TNILLIAHYSFLSHTSTTRAAYFAYLL--CVCVSSISCCIDPLIYYYASSECQRYVY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96379236; PubMed=8784787; MEDLINE=96379236; PubMed=8784787; MEDLINE=96379236; R., Kuo W. L., Piper M., Connolly A., Shi Y.P., Wu R., Lin C.C., Coughlin S.R.; Establin S.R.; Conserved structure and adjacent location of the thrombin receptor and protease-activated receptor 2 genes define a protease-activated receptor gene cluster."

Mol. Med. 2:349-357(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7fm_1; 1.
PRNSTS; PP00037; GPCRENDODESN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
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Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                      384 SILCCKESSDPSSSNSGQLMASKMDTCSSNLANSIY 420
                                                      318 GILKLKGSSSSSSSSSSTPGKASSETPSITQARGSMF 354
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U36756, AAB38308.1; JOINED.
U55076, AAB00198.1;
U55075, AAB00198.1; JOINED.
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HSSP;
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SEQUENCE FROM N.A. Straington D.P., Chung M.-W., Lee K.L., Poel Nickerson D.A.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

reveals a

MEDLINE-91168254; PubMed=1672265; T.Y. Coughlin S.R.; Mholecular cloning of a functional thrombin receptor proteolytic mechanism of receptor activation."

SEQUENCE FROM N.A.

NCBI_TaxiD=9606;

proteolytic mechanism of Cell 64:1057-1068(1991).

Butheria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 WRGCLLTLLMLVAVVVCFSPYHLNIKQFMARGMLHLPSCAERRAFLLSLQATVALMNMNC 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 CMEYSSMESVLGLPLMVLVAF-AIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRH 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 CHDVLSENLMQGFYSYYFSAFSAİFFLVPLIVSTVCYTSIIRCLSSSA-----VANRSKK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 SRALFLSAAVFCIFIVCFGPTNV----LLIVHYLFLSDSPGTEAAYFAYLLCVCVSSVSC 369
                                                                                                                                                                                                                                                                                                                                                                                                       62 INCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLM 121
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tive 63; Mismatches 163; Indels 14; Gaps
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  FOR RECEPTOR ACTIVATION
                     PROTEINASE ACTIVATED RECEPTOR 1.
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G -> Y (IN REF. 1).
R -> G (IN REF. 1).
V -> L (IN REF. 1).
S -> T (IN REF. 1).
395PD64FAES2C9BF CRC64;
                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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6 (POTENTIAL).
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                        19.0%; Score 357; DB 1; 28.6%; Pred. No. 1.8e-18;
                                                                                                                                                              7 (POTENTIAL).
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47790 MW;
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es 96, Conservative
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430 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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MEDI-TRE-99318093; PubMed=10391209;
Cardill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Priedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Protease-activated receptors 1 and 4 mediate activation of human platelets by thrombin.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99178892; PubMed-10079109;
Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
Coughlin S.R.;
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Nat. Genet. 22:231-238(1999).
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PARI_HUMAN STANDARD; PRT; 425 AA.
P25116; 096RF7; 09BUN4;
01-May-1992 [Rel. 22, Created)
41-May-1992 [Rel. 22, Created)
15-SEP-2003 [Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Proteshase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
(Coagulation factor II receptor)
(Coagulation factor II receptor)
FOR OR PARI OR TR OR CF2R.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R GO; GO: 0005794; C: Golgi apparatus; TAS.

R GO; GO: 0005887; C: Integral to plasma membrane; TAS.

GO; GO: 0005887; C: Integral to plasma membrane; TAS.

GO; GO: 0005887; C: Integral to plasma activity; TAS.

GO; GO: 0005912; F: treceptor binding activity; TAS.

R GO; GO: 0006915; P: papoptosis; TAS.

R GO; GO: 0006919; P: caspase activity; TAS.

R GO; GO: 0006919; P: caspase activity; TAS.

R GO; GO: 0007275; P: paverloment; TAS.

R GO; GO: 0007275; P: pregulation; TAS.

R GO; GO: 0007125; P: pregulation of cell cycle; TAS.

R GO; GO: 0007125; P: pregulation of cell cycle; TAS.

R GO; GO: 0007125; P: pregulation of cell cycle; TAS.

R GO; GO: 0007125; P: pregulation of cell cycle; TAS.

R GO; GO: 0007126; P: pregulation of cell cycle; TAS.

R GO; GO: 0007126; P: pregulation of cell cycle; TAS.

R GO; GO: 0007126; P: pregulation of cell cycle; TAS.

R GO; GO: 0007260; P: pregulation of cell cycle; TAS.

R GO; GO: 0007260; P: pregulation of cell cycle; TAS.

R GO; GO: 0007260; P: pregulation of cell cycle; TAS.

R GO; GO: 0007260; P: pregulation of STAT protein; TAS.

R PRINTS: PRO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_2; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROSITE; PSO0237; G-PRRTEIN_RECEP_F1_1; 1.

R PROOF CONTREIN_RECEP_F1_1; 1.

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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (ALSNP. 5893).
/FTIG=VAR 014167.
L -> V (IN REF. 1).
A -> V (IN REF. 3).
C -> S (IN REF. 1).
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PROTEINABE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
ASP GLU-RICH (ACIDIC).
CLEAVAGE (BY THROMBIN).
BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                         EMBL, M62424; AAA36743.1; -.
EMBL, AF391809; AAK69768.1; -.
EMBL, BC002464, AAH02464.1; -.
PIR, A37912, A37912.
PDB, INRN, 31-MAY-94.
PDB, INRQ; 31-MAY-94.
PDB, INRQ; 31-MAY-94.
MM, 187930; -.
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                                                                                     98 SSWLTLFVPSV-YTGVFVVSLPINIMAIVVFILKOKKYRKPAVVYMLHLATADVLFVSVLP 156
                                                                                                                                                       328 P--TNVLLIAHYSFLSHTSTTEAAYFAYLL--CVCVSSISCCIDPLIYYYASSECQRYVY 383
                                                                                                                                      85 GRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTA 144
                                                                                                                                                                                                                                                                                                                                                  258 PYHLNIKQFWARGMLHIPSCAERRAFLLSLQATVALMNMNCGITFIIYFFASTHYRKWLL 317
                                                                                                                                                                                                         GRARLYCVAIWTLVLLQTMPLLLIMPMTKPLVGKLACMEYSSMESVLGLPLM------VLV
                                                                                                                                                                                                                            AF-AIGFCGPVGILLSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFS
                                                                   SQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALP
                                 Gaps
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MEDLINE=20193820; PubMed=10729156;
MEDLINE=20193820; PubMed=10729156;
MEDLINE=20193820; PubMed=10729156;
MITHE Genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
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or send an email to ...

or send an email to ...

JR EMBL; AP198100; AAP44550.1; ...

DR InterPror; IPRO00276; GPRRHODOPSN.

DR PROSITE; PS00237; GPRRHODOPSN.

DR PROSITE; PS00237; GPROTEIN RECEP F1.1; 1.

DR PROSITE; PS00262; GPROTEIN RECEP F1.2; 1.

RW G-POTCHIN COUpled receptor; Transmembrane; Glycoprotein.

FT DOMAIN

TRANSMEM 21 41 10 TRANSMEM POTENTIAL).

TRANSMEM 21 41 20 CYTOPLASMIC (POTENTIAL).

S3 73 2 (POTENTIAL).

S3 73 2 (POTENTIAL).

S4 POTENTIAL).

S 3 (POTENTIAL).
                               21;
 Length 425;
                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       318 GILKLKGSSSSSSSSSSTPGKASSETPSITQARGSMF 354
Query Match
18.8%; Score 352.5; DB 1;
Best Local Similarity 29.7%; Pred. No. 3.8e-18;
Matches 100; Conservative 57; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annocation update)
G-protein coupled receptor homolog FPV206.
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Fowlpox virus (FPV)
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NCBI_TaxID=10261;
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                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 KIACACTWVIILVPMSSILFVSTISSDHETKIRCMEYNKVGDSMYLPPWVTIVMCFIGFV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 IPPAMMAISYSAVCYTVLSG-----ISKSTRSYRTCKLVACILTEFVICFLPYHASVIS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 Y----MIHIITSKTVLCENVSYYQMLLHATQCLMKLNCCMDPIIYLFVSSYKSKAKSNSI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 VCYVLGSSWPPGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 RLVCVAIWTLVLLQTMPLLLMPMT-KPLVGKLACMEYSSMESVLGLPLMVLVAFA-IGFC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 FMARGMLHLPS-----CAERRAFLLSLQATVALMNWCGITPIIYFFASTHYRKWLLGIL 320
                                                                                                                                                                                                                                                                                                                                                                                             19 SLAVVILLIFSSSLILNISALVIGFYTTAPGPMK-----MYLINLIVSDILFTVTLPLKKI 73
                                                                                                                                                                                                                                                                                                                                                                     34 SLFYTALLVFSA--LGNILALCL----TCQKSRKINCTGIYLVHLAVSDLLFTVALPGRV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor.",

J. Biol. Chem. 267:16975-16979 (1992).

J. Biol. Chem. 267:16975-16979 (1992).

J. FUNCTION: High affinity receptor for activated thrombin coupled to G proteins that stimulate phosphoinositide hydrolysis.

J. SUBCELLULAR LOCATION: Integral membrane protein.

FIN: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 DYYYYFFNWRWGEMACRIMSFLSYINTYVSINFWTWISVNRYYAVTRPHKYNSRDNIWRT
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TISSUE-Acrtic smooth muscle;

MEDLINE=92381002; PubMed=1324917;

Zhong C., Hayzer D.J., Corsen M.A., Wick K., Runge M.S.;

"Molecular cloning of the rat vascular smooth muscle thrombin receptor. Evidence for in vitro regulation by basic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                   ; Score 341; DB 1; Length 308;
; Pred. No. 1.8e-17;
55; Mismatches 129; Indels
                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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  CYTOPLASMIC (POTENTIAL)
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01-AUG-1992 (Rel. 23, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                              35375 MW;
                                                                                                                                                                                                                                                                                   18.2%;
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PARI RAT
AC P26824,
DT 01-AUG-199
DT 28-FEB-200
DE Proteinase
GN Rattus nox
OC Mammalia,
OX NCBI_TAXII
CO MAMMALIA
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 CTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPIASMIC (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
POLY-PRO.
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
                                                                                                                                                                      EMBL; M61642; AAA42274.1;

PIR; A43448; A43448

HSSP; P34996; 1DDD

HIGEPPO: IPRO00276; GPCR_Rhodpsn.

PEAM; PRO0001; 7tm 1; 1.

PRINTS; PRO0237; GPCRRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.

PROSITE; PS00262; GPOTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; SIGNAL

SIGNAL

POTENTIAL.

POTENTIAL.

POTENTIAL.
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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PROTBINASE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)
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Query Match
Best Local
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                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIATE-94195429; PubMed=8145852;
MEDIATE-94195429; Tubmed=8145852;
Gerszten R.E., Chen J., Ishii M., Ishii K., Nanevicz T.,
Turck C.W., Vu T.-K.H., Coughlin S.R.;
"Specificity of the thrombin receptor for agonist peptide is defined by its extracellular surface.",
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 300:100-031. Migh affinity receptor for activated thrombin coupled ---- FUNCTION: High affinity receptor for activated thrombin coupled G proteins that stimulate phosphoinositide hydrolysis.
---- SUBCELLULAR LOCATION: Integral membrane protein.
---- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
---- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
K-A: LACK OF ACTIVATION BY THROMBIN
D5163F56APE12372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IS1667.

Pfam; PP00001; 7tm 1; 1.

PRINTS; PR00237; GPCRENDODSN.

PROSITE; PS00237; GPCRENDODSN.

PROSITE; PS50262; GPROTEIN RECEP FL_1; 1.

PROSITE; PS50262; GPROTEIN RECEP FL_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
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PROTEINASE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                    (Rel. 33, Created)
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PIR; I51667; I51667.
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                                                                              STANDARD;
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                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                              01-FEB-1996
01-FEB-1996
28-FEB-2003
                                                                                 PAR1 XENLA
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SEQUENCE
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                                                                                                                                                                                                                                                                DILIFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                          207 MHSLSWRTMSRAYMACSFIWLISIASTIPLLVTEQTQ----KIPRLDITTCHDVLDLKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 KDFYIYYPSSFCLLFFFUPFIITTICYIGIIRSLSSSSIENSC-----KKTRALFLAUVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVAVVVCESPYHLNIKQFMARGMIHLPSCAERRAFLLSLQATVALMMMVGITPIIYFFA
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                                                                                                                                   16 TKIKDINVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Neural plate;
MEDINE=979484734; PubMed=9139711;
Bogdanov Y.D., Dale L., King B.F., Whittock N., Burnstock G.;
"Early expression of a novel nucleotide receptor in the neural plate
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEACH. CHEM. 272:12583-12590(1997).

BIOL. CHEM. 272:12583-12590(1997).

FUNCTION: RECEPTOR FOR EXTRACELLIDAR ATP, UTP, CTP, GTP AND ITP.

THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

MAY PLAY A KEY ROLE IN THE BARLY DEVELOPMENT OF NEURAL TISSUE.

SUBCELLULAR LOCATION: Integral membrane protein.

SUBCELLULAR BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                   25;
17.7%; Score 332.5; DB 1; Length 420; 26.6%; Pred. No. 9.7e-17; ive 74; Mismatches 155; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STHYRKWLLGILKLKGSSSSSSSSSSTPGKASSETPSITQARGSMF 354
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
P2Y purinoceptor 8 (P2Y8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00001; 7tm 1; 1.
PRINTS: PR00231; GFCMFHODPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; PROSITE; PSC0262; G PROTEIN RECEP F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR000276; GPCR_Rhodpsn.
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                                                                       Conservative
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J. Biol. Chem. 272:12
                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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ÆDLINE=97432828; PubMed=9286708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLAC- 180
                                                                                                                                                                                                                                                                                                                                                                                      PYL--PMKLLMNLTNDTEDICVPDEGFKFLLLPVSYSAVFWVGLPLNIAAMWIFIAKMRP 74
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                                                                                                                                                                                                                            193 BY SIMILARITY.
26 N-LINKED (GLCNAC. . .) (POTENTIAL).
29 N-LINKED (GLCNAC. . .) (POTENTIAL).
62024 MW, B2CF24812F3C19F2 CRC64;
                                                                                                                                                                                                                                                                                                                                 28;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
131.
                         1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
 Transmembrane; Glycoprotein. EXTRACELULAR (POTENTIAL).
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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P2Y6 HUMAN
Q15077, Q15754;
Q1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 42, Last annotation update)
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 protein coupled receptor;
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537 AA;
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P2X6 AC 01507
DT 01-NC
DT 15-SE
DD P2XY E
DN P2XY E
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[2] SEQUENCE FROM N.A

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Strausberg R.L., Feingold B.A., Grouse I.H., Derge J.G.,

REDLINE=2238815; PubMed=12477932;

Strausberg R.L., Feingold B.A., Grouse I.H., Derge J.G.,

Riausner R.D., Collins F.S., Magner I., Schaefer C.P., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

B. Graplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzuny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schutz Z. J.,
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                                                                                                                                                                                                                                                             Maier R., Glatz A., Mosbacher J., Bilbe G.; "Cloning of P2Y6 CDNAs and identification of a pseudogene: comparison of P2Y receptor subtype expression in bone and brain tissues."; Blochem. Biophys. Res. Commun. 237:297-302(1997).
                                                               "Chromosomal localization of the human P2y6 purinoceptor gene and phylogenetic analysis of the P2y purinoceptor family."; Genomics 44:127-130(1997).
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                         Somers G.R., Hammet F., Woollatt E., Richards R.I., Southey M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
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Maier R., Glatz A., Mosbacher J., Bilbe G.;
Blochem. Biophys. Res. Commun. 240:298-302(1997)
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MEDLINE=97415792; PubMed=9268704;
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EMBL; U52464; AAB03572.1; -.
EMBL; AF007892; AAB80713.1; -
EMBL; AF007891; AAB80712.1; -.
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    CCR8 OR CMKBR8 OR TER1.
               Mus musculus (Mouse)
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                                                              SEQUENCE FROM N.A.
                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTARED----PVT-SRKGR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 HWRGCLLTLLMLVAVVVCFSPYHLNIKQFMA-RGMLHLPSCAERRAFLLSLQATVALMNM 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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                                                                                                                                                                                                                                                                                                                                                                                                           14 PPTTC------VYRENFKOLLLPPVYSAVLAAGLPLNICVITQICTSRRALTRTAVYT
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                                                                                                                                                                                                                                                                                                                                                                             34;
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                                                                                TAS.
to IP3 second
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CRR-8) (CCR-8)
EMBL; AF218005; AAG17247.1; -.

R EMBL; AF49820; AAM18129.1; -.

R EMBL; BC000391; AAH00391.1; -.

R EMBL; BC000391; AAH00391.1; -.

R EMBL; BC000391; AAH00391.1; -.

R EMBL; BC000391; AAH00391.1; -.

R EMBL; BC0091; UC4800.

R GENEW; HGNC: 8543; P2RV6.

R GO; GO: 0007200; P: G-protein signaling, coupled to IP3 second InterPro; IPR00276; GPR_Rhodpsn.

R GO; GO: 0007200; P: G-protein signaling, coupled to IP3 second InterPro; IPR00270; GPR_Rhodpsn.

R PROSTIS: PR00237; GPRRHODOPSN.

R PROSTIS: PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.

R PROSTIS: PS00237; GPROTEIN RECEP_F1_2; 1.

T PANGNAIN 1 27 EXTRACELLULAR (POTENTIAL).

T TRANSMEM 28 1 CTTOPLASMIC (POTENTIAL).

T TRANSMEM 49 62 CTTOPLASMIC (POTENTIAL).

T TRANSMEM 63 83 2 (POTENTIAL).

T TRANSMEM 102 122 3 (POTENTIAL).

T TRANSMEM 102 122 3 (POTENTIAL).

T TRANSMEM 102 122 3 (POTENTIAL).
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                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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MISSING (IN REF. 2).
AAD6C55A43818107 CRC64;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immundl. 161;547-551(1998).
-!- FUNCTION: RECEPTOR FOR THE TCA-3 CHEMOKINE.
-!- SUBCELLULAR LOCATION. Integral membrane protein.
-!- SIMCELLULAR: PELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
rub muzotus (Arzos.).
Bukaryota; Metazos.).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; Z98206; CAB10895.1; --
EMBL; Z98206; CAB10895.1; --
EMBL; ARCO1277; AACS7598.1; --
EMBL; ARCO1277; AACS7598.1; --
EMBL; ARCO1277; ACC Chemokine receptor activity; IDA.
GO; GO:0005315; F:C-C chemokine activity; IPI.
GO; GO:0005315; F:C-C chemokine activity; IPI.
GO; GO:0005315; F:C-C chemokine activity; IPI.
FERM; FRO0001; TENENGER; CARNONON:
FRINTS; PRO1037; GPCR.HODOPSN.
FROSITE; PS00237; GPCR.HODOPSN.
FROSITE; PS00237; GPCR.HODOPSN.
FROSITE; PS00237; GPROTEIN RECEP. F1.1; 1.
FROSITE; PS00237; GPROTEIN RECEP. F1.2; 1.
G-PROSITE; PS00237; GPROTEIN RECEP. F1.2; 1.
FROSITE; PS00237; GPROTEIN RECEP. F1.2; 1.
FROSITE; PS00237; GPROTEIN RECEP. F1.2; 1.
FROSITE; PS00225; GPROTEIN RECEP. F1.2; 1.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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TGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACV 124
                  -----LILLMLVAVVVCFSPYHLNIKQFMARGMIH----LPSCAERRAFLLSLQATV 291
                                                                                                                                                                                                                              229 HNRTRAIKLVILVVIVSLLFWVPF--NVALFLT--SLHDLHILDGCATRQRLALAIHVTE 284
                                                                                                                                                                                                                                                                                                   285 VISFTHCCVNPVIYAFIGEKFKKKHLMDVFQKSCSHIFLYLGRQMPVGALERQLSSNQRSS 344
                                                                   SVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTWPLLLMPMTKPLVGKLACMEYS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CRR-8) (CC-CKR-8) (GPR-CY6)
(GPRCY6) (Chemokine receptor type 8 (C-C CRR-8) (CRR-LI) (TER1) (CMKBRL2) (CC-Chemokine receptor CHEMR1).
CCR8 OR ORMERS OR CRRL1.
                                                                                                                                    SMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCL-
                                                                                                                                                                                                                                                                             292 ALMNWNCGITPIIYFFASTHYRKWLL-------GILKLKGSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=97351133; PubMed=9207005; Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M., Combadiere C., Modi W., Bonner T.I., Murphy P.M.; Identification of CCR8: a human monocyte and thymus receptor for the CC chemokine I-309."; J. Exp. Med. 186:165-170(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A. MEDIME 9469461; MEDIME 30129363; PubMed 9469461; MEDIME 99129363; PubMed 9469461; Medimer D., Zaballos A., Marquez G., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G., "Identification of CCR8 as the specific receptor for the human beta-chemokine 1-309: Gloning and molecular characterization of murine CCR8 as the receptor TCA-3."; CCR8 as the receptor TCA-3."; J. Immunol. 160:1975-1981(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloining and chromosomal mapping of a novel human gene, ChemR1, expressed in T lymphocytes and polymorphonuclear cells and encoding a putative chemckine receptor."; Eur. J. Immunol. 26:3021-3028(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97040707; PubMed=8886020;
Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
"Molecular cloning and RNA expression of two new human chemokine
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MEDLINE=97131825; PubMed=8977299;
Samson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
Parmentier M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 227:846-853(1996).
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                                                                                                                                     "Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor.";

Eur. J. Immunol. 28:582-588(1998).

-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-beta and SCYA1/TARC. May regulate monocyte chemotaxis and thymic cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAN, DV.1637, DV.1637, C. integral to plasma membrane, TAS.

GO; GO:0015026; R:coreceptor activity; TAS.

GO; GO:000155; P:cell adhesion, TAS.

GO; GO:0007155; P:cell adhesion, TAS.

GO; GO:0007204; P:chemocaxis; TAS.

GO; GO:0007186; P:c-protein coupled receptor protein signalin. .; T.

InterPro; IPR000269; C. chemkine8.

InterPro; IPR000269; GPGR_Rhodpsn.
                                                                                                                                                                                                                                               -i- SUBCELLUTAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                          MEDLINE-98180363; PubMed-9521068;
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti
Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEQUENCE FROM N.A.
Nakajima T., Yoshida R., Harada S.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL, AF005210; AAB62547.1; -.
PIR; JC5067; JC5067.
Genew; HGNC:1609; CCR8.
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PRINTS; PR00237; GPCRRHODOPSN
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EMBL; U62556; AAB05542.1; -.
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EMBL; Y08456; CAA69712.1; -.
EMBL; D49919; BAA23387.1; -.
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305
106
355 AA;
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Matches 89
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                           147 IRMGTTLCLAVWITAIMATIPLLVFYQVASEDGVLQCYSFYNQQT---LKWKIFTNFKOM
                                                                                                                                                                                                                                                                                                                204 ILGLLIPFIFECYIKILHQLKRCQNHNKT------KAIRLVLIVVIASLLFWVP
                                                                                                                       144 AGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAFAIG
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     QTVKIFLRSLFYTALLVFSALGN--ILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Receptor for cysteinyl leukorrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity). SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S., Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 1 (CystrR1).
CYSLTR1 OR CYSLT1.
Sus scrofa (Rig).
Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae; Sus.
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR01533; GPCRHHODOPSN.
PROSITE; PS00237; GPRCHHODOPSN.
PROSITE; PS02237; GPRCTEIN RECEP F1 2; 1.
PROSITE; PS02262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
1 (POTENTIAL).
2 (POTENTIAL).
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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Power C.A., Mayer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
Proudfoot A.E.I., Wells T.N.C.,
"Molecular cloning and functional expression of a novel CC chemokine
"receptor cDNA from a human basophilic cell line.";
J. Biol. Chem. 270:19495-19500(1995).
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Catarrhini; Hominidae; Homo.
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P51679; Q9ULV6; Q9ULV7;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last samotation update)
C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4)
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7 (POTENTIAL).
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CYTOPLASMIC
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Homo sapiens (Human)

Bukaryota, Metazoa; Chordata; (Mmmalia; Eutheria; Primates; (MCBI_TAXID=9606;
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-1. FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES
TARC/SCYA17 AND MOC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY G(I) PROTEINS WHICH ACTIVATE A PHOSPHATDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOATRACTANT
HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A
CORECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A
CORECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A
CORECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES IN THE CNS, COULD
MEDIATE HIPPOCAMPAL-NETRON SURVIYAL.

-1. SUBCELLULAR LOCATION: Integral membrane protein.

-1. SUBCELLULAR LOCATION: Integral membrane protein.

-1. SUBCELLULAR LOCATION: Integral membrane protein.

-1. SUBCELLULAR LOCATION: Integral membrane protein.

-1. SUBCELLULAR LOCATION: Integral membrane Tevels, IN THE SPLEEN
AND BASOPHILLS, AND IN PLATELETS; AT LOWER LEVELS, MOSTLY THE
CONSE SPRESSING THE CUTANEOUS LAND MEMORY T CELLS, MOSTLY THE
CONSE SPRESSING THE CUTANEOUS LAND MEMORY T CELLS.

-1. PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDICES
CONSE SPRESSING THE CUTANEOUS LAND SOCKIARY ARTERY ENDOTHELIAL CELLS.

-1. PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDICES
CONSE SPRESSING RECEPPOR KINASES 1 AND 2.

-1. SIMILARITY: BELONGS TO PAMILY 1 OF G-PROTEIN COUPLED RECEPPORS.
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98104168; Pubmed=9430724; Inai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R., Yoshie O., Gray P.W.; William of the CC "Macrophage-derived chemokine is a functional ligand for the CC
                        Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H., Hizał K., Tokkunaga K.;
Hizał K., Tokkunaga K.;
"Now variations of human CC-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
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MEDLINE=20219238; PubMed=10754297;
Inngjerdingen M., Damaj B., Maghazachi A.A.;
"Human NK cells express CC chemokine receptors 4 and 8 and respond to thymus and activation-regulated chemokine, macrophage-derived chemokine, and I-309.";
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Nature 400:776-780(1999).
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Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yosh
"The T cell-directed CC chemokine TARC is a highly specific
biological ligand for CC chemokine receptor 4.";
J. Biol. Chem. 272:15036-15042(1997).
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MEDLINE=21040311; PubMed=11196669;
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EMBL; AB023889; BAA86966.1; --
EMBL; AB023891; BAA86967.1; --
EMBL; AB023891; BAA86968.1; --
EMBL; AB023892; BAA86969.1; --
EMBL; AB023892; BAA86969.1; --
EMBL; AB023892; BAA86969.1; --
EMBL; AB023892; BAA86969.1; --
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MIM; 604836; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 -NIVLFLETLVELEVLODČTFERYLDYALOATETLAFVHČCLNPILYFFLGEKFRKYILO 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 ---YYAADQWVFGLGLCKMISWMYLVGFYSGIFFVMLMSIDRYLAIVHAVFSLRARTLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 ELFLPPL-YSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLLFVFSLPFWG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 ARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAFAIGFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 PVGIILSCYMKI--TWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCF----SPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 LNIKQFMAR--GMLHIPSCAERRAFILSIQATVALMNNNCGITPIIYFFASTHYRKWLL-
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004580; P:chemokine receptor activity; TAS.
GO; GO:0004535; P:chemokine; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0006554; P:inflammate response; TAS.
InterPro; IPRO0276; GPCR_Rhodpsn.
PRIMTS; PRO0277; GPCRRHODPSN.
PROSITE; PS00237; GPCRRHODPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1.1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 KIFLRSLFYTALLVFSALGNILALCLTCOKSRKINCTGIYLVHLAVSDLLFTVALP--GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 VVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.2%; Score 322.5; DB 1; Length 360; Best Local Similarity 28.3%; Pred. No. 4.3e-16; Matches 93; Conservative 58; Mismatches 131; Indels 47;
                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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(POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
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February 19, 2004, 19:29:05; Search time 41 Seconds (without alignments) 2265.828 Million cell updates/sec
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1876
1 MIKLGPYFTPPTKIKTKIKD.....SETPSITQARGSMFLAEHVV 360
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Nansey homo sapien	Q8vhp3 cavia porce	Q9byx5 homo sapien	28iv19 homo sapien	29hlc0 homo sapien	Q91zh4 rattus norv	Q8hzn4 cercopithec	28hzn5 macaca mula	8hzn6 pongo pygma	9myj8 callithrix	Q8mjw8 canis famil	8iuz1 homo sapien	Q8hzn8 pan troglod	8ne10 homo sapien	Q8by68 mus musculu	28hzn7 gorilla gor
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SUMMARIES			~				***									60	
SUM	a	Q8N5S7	Q8VHP3	Q9BYX5	Q81V19	Q9H1C0	Q91ZH4	Q8HZN4	QBHZNS	9NZH8Ö	Q9MYJ8	Q8MJW8	QBIUZI	Q8HZN8	OBNE10	QBBY68	Q8HZN7
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40	Query Match	20.7	17.7	17.3	17.2	16.9	16.8	16.7	16.6	16.5	16.5	16.4	16.3	16.3	16.3	16.3	16.2
	Score	387.5	332.5	324	323	316.5	314.5	313.5	310.5	309.5	309	308.5	306.5	306.5	306.5	305	304.5
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	O57466 meleagris g	OBPWCO WAS MUSCUlu		Q9qwn6 mus musculu	Q9de05 raja erinac	Q9erk9 mus musculu	Q8k1z6 mus musculu	Q9jii9 rattus norv	Q8bkk1 mus musculu	att	Sn	ยกเ	Q8blg2 mus musculu	Q8n6t6 homo sapien	Q8byil mus musculu	Ospado mas mascala	O93237 cyprinus ca	Q9bxc0 homo sapien	Q8qfr6 xenopus lae		Q98u14 brachydanio	Q8k3m7 mus musculu		7 xeno	Q8bvf1 mus musculu	SUM 8	Q8cbj0 mus musculu	Q9pvy7 anguilla an
093239	057466	QBBMC0	Q8HZN3	9NMQ6Q	Q9DE05	O9ERK9	Q8K1Z6	GIIC6Ö	QBBKK1	09JIZ0	Q91WIO	Q8R528	QBBLG2	Q8N6T6	QBBYI1	QBBUD0	093237	Q9BXC0	Q8QFR6	Q9PTF7	Q98U14	Q8K3M7	Q8C131	Q90X57	Q8BVF1	Q8BHB8	Q8CBJ0	Q9PVY7
13	13	디	9	디	13	T	11	11	11	17	11	11	11	4	11	11	13	4	13	13	13	17	11	13	11	11	11	13
342	374	344	355	367	357	328	331	367	370	362	362	309	370	350	375	365	372	346	360	353	377	359	343	361	377	359	354	359
16.2	16.2	16.2	16.0	16.0	16.0	15.8	15.7	15.7	15.6	15.5	15.5	15.4	15.4	15.4	15.4	15.4	15.4	15.3	15.3	15.3	15.2	15.2	15.1	15.1	15.1	15.1	15.0	15.0
304	304	303.5	300.5	300	299.5	296	294.5	294.5	293.5	290.5	290.5	289.5	289.5	288.5	288.5	288	288	287	287	286.5	286	284.5	283	283	283	282.5	281	281
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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96 WPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIW 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 TLVLLQTMPLLLMPMTKPLVGKLACME-YSSMESVLGLPLMVLVAFAIGFCGPVGIILSC
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.7%; Score 387.5; DB 4; Length 339; Best Local Similarity 30.2%; Pred. No. 1.3e-27; Matches 94; Conservative 57; Mismatches 143; Indels 17
                                                                                                                                                                                               TISSUE-Brain, and Lung;
Straubberg R.;
Straubberg R.;
Submitted (Unv.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031653; AAH31653.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PR00001; 7Fm.ml; 1. -.
PRINTS; PR00037; GPCRHODDPSN.
PROSITE; PS00237; GPROTEIN RECEP_FI_1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_FI_2; 1.
                                                                                                                                                                                                                                                                                                                                                                       339 AA; 37860 MW; BB0CAFD0FC371D63 CRC64;
                                          Q8NSS7;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
G protein-coupled receptor 17.
                             339 AA
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                               Q8N557
RESULT 1
              Q8N5S7
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Query Match
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                     Q9BYX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 SDLLFVLSLPFWG----YYAADQWVFGLGVCKMISWIYLVGFYSGIFFIVLMSIDRYLAI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDLLFTVALP--GRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 VCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 PLMVLVAFAIGFCGPVGIILSCYMKI--TWKLCSTAREDPVTSRKGRHWRGCLLTLLLMLV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 VLSSLEINILGEVIPLGIMLFCYSMIRTLQHCKSXKKNKAVK--------MIF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 AVVVCF----SPYHLNIKQFMARGMLHLPSCAERRAFLLSLQATVALMNMVCGITPIIYF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 VVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKAS----HHALVSLAVAFTFPFITTVTC 211
                                                   267 ASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRLKGPPPSFEG 326
                                                                                 275 PSCAERRAFLLSLQATVALMMNCGITPIIYFFASTHYRKWLLGIL---KLKG---SSSS 328
                                    YMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKOFMARGMLHL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTKIKDINVESQTVKI FLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAV
                                                                                                                                                                                                                                                                                                                                                 Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,
Hodge M.R., Williams T.J., Pease J.E.,
The identification, characterization and distribution of guinea pig
CCR4 and epitope mapping of a biocking antibody.",
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF431971, AAL57488.1,
PEARL, PF401001, 7tm 1, 1.
PRINTS, PR0001, 7tm 1, 1.
PRINTS, PR0017, GPRCRHODOPSN.
PROSITE; PS50262; GPRCRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                       CC-chemokine receptor 4.
Gavia porcellus (Guinea pig).
Eukaryots, Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 332.5; DB 11; Length 361; 27.1%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AA; 41064 MW; 9304E897D4FD6839 CRC64;
                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                               361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASTHYRKWLLGILK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Conservative
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                329 SSSSSSTPGKA 339
                                                                                                                                                      327 KTNESSLSAKS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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Best Local 8
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                                                                                                                                                                                                               ОВVНР3
                                                                                                                                                                                         RESULT 2
Q8VHP3
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143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 YHLNIKQFMARGMLHLPSCAERRAFLLSLOATVALMNMNCGITPIIYFFASTHYRKWL-- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                  147 IRMGTTLCLAVMLTAIMATIPLLVFYQVASEDGVLOCYSFYNQOT---LKWKIFTNFKMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 ILGLLIPFTIFMFCYIKTLHQLKRCQNHNKT------KAIRLVLIVVIASLLFWVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 FCG---PVGIILSCYMKITWKL--CSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 QIVKIFLRSLFYTALLVFSALGN.--ILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 PGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Bukaryotas Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
NCBI_TAXID=9606;
                                                                                                                                              Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                             DeVries M.E., Xu L., Kelvin A.A., Kelvin D.J.; and CCR8 "Identification and characterization of the CX3CR1 and CCR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 17.3%; Score 324; DB 4; Length 35 Local Similarity 26.4%; Pred. No. 1e-21; les 89; Conservative 65; Mismatches 145; Indels
                                                        Last sequence update)
Last annotation update)
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                                      Created)
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                                01-UUN-2001 (TrEMBLrel. 17
01-UUN-2001 (TrEMBLrel. 17
01-WAR-2003 (TrEMBLrel. 23
CC chemokine receptor 8.
CCR.
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  PRELIMINARY;
                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI TaxID=9606;
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Submitted (APR-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTLVLLQIMPLILMPMTXPLVGKLACME----YSSMESVLGLPLMVLVAFAIGFCGPVG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFMAR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 STLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVADLLCVCTLPLRVVYYVHK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 SSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMLH--LPSCAERRAFILSLQATVALMNNNCGITPIIYFFASTHYRKWLLGILKLKGSSS
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative G protein-coupled receptor 92 (Putative G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MIDLINES-201.7346, PubMed=11062477;
White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
Attocsomal dominant hypophosphataemic rickets is associated with
mutations in FGP23.";
Nat. Genet. 26:345-348(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                        17.2%; Score 323; DB 4; Length 337;
29.9%; Pred. No. 1.2e-21;
cive 50; Mismatches 150; Indels 20;
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MEDLINE=21458557; PubMed=11574155,
Lee D.K., Nauyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko
Lee J.K., Byans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
"Identification of G protein-coupled receptor genes from the
                                                                                     Straubberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035750; AAH35750.1; -..
Hypothetical protein.
SEQUENCE 337 AA; 38486 MW; B9B09CE0FD305245 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                          Local Similarity 29.99
Les 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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GRP92 OR GPR93 OR GPCR.
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                                                                       TISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J., Bacon K.B., Feng L., "Monomuclear cell-infiltrate inhibition by blocking macrophage-derived chemokine results in attenuation of developing crescentic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LHLVVYSLVLAAGLPLNALALMVFLRALRVHSVVSVYMCNLAASDLLFTLSLPVRLSYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVC
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Rattus norvegicus (Rat).

Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 372;
                                                                                                   Straubberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A272207; CAC03715.1] ...
EMBL; AR41112; AAL26483.1; ...
EMBL; AB083600; BAB9313.1; ...
EMBL; AB083500; BAB9313.1; ...
EMBL; AB083500; BAB9313.1; ...
EMBL; AB083500; BAB9313.1; ...
EMBL; AB000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00027; GPCRPHODPSN.
PROSITE; PS00237; GPCRPHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 316.5; DB 4; Length
; Pred. No. 5.2e-21;
59; Mismatches 150; Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF432872; AAL30398.2; -.
to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA; 41346 MW; BA35709084BB6D84 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
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315 HRARTSATNGTRAALAQSERSAVT 338
                                                      SEQUENCE FROM N.A.
TISSUE=Primary B-Cells from Tonsils;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.9%;
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PRELIMINARY;
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01-MAR-2003
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                                   317
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYHL-NIKQFMARGMLHLPSCAERRAFLLSLQATVALMNWNCGITPIIYFFASTHYRKWL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 AGR--ARLVCVAIWTLVTLQTMPLLLMPMT-KPLVGKLACMEYSSMESVLGLPLMVLVAF 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRYLVKFVCLSIWGLSLLLALPVLLFRRTVYPTYISPVCYEDMGNNTAKWRWVLRILPQ 211
                           9
                                                                                                87 VVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGR 146
                                                                                                              147 ARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAFAIGFCG 206
                                                                                                                                                                GVITSLITWSVAVFASLPGILFSTCDTENNHTYCKTQYSVNSTTWKVLSSLEINVLGLVI 213
                                                                                                                                                                                                 PVGIILSCYMKI--TWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCF----SPYH 260
                                                                                                                                                                                                               PLGIMLFCYSMIIRTLRHCK-----NEKKNRAVR------MFAVVVLFLGFWTPY- 258
                                                                                                                                                                                                                                                  LNIKQFMAR--GMLHLPSCAERRAFILSLQATVALMNNNCGITPIIYFFASTHYRKWLLG 318
                                                                                                                                                                                                                                                               37 ESLEINKYFVVIIYALVFLLSLLGNSLVMLVILHSRVGRSVTDVYLLNLAMADLLFALTL 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 AIGFCGPVGIILSCY---MKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFS
                                                               39 EVFLPPL-YSLVFLLGLFGNSVVVLVLFKYKRLKSMTDVYLLALAISDLLFVLSLPFWG-
                                                 29 KIFLRSLFYTALLVFSALGNILALCLTCOKSRKINCTGIYLVHLAVSDLLFTVALP--GR
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                          Gaps
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01-MRA-2003 (TrEMBLrel. 23, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
101-MRA-2003 (TrEMBLrel. 23, Last annotation update)
11-terleukin 8 receptor B CXCR2.
12-croopithecus pygerythrus.
13-croopithecus pygerythrus.
14-croopithecus pygerythrus.
15-croopithecus primates; Catarrhini; Cercopithecidae;
16-croopithecidae;
17-croopithecidae;
17-croopithecidae;
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                          45;
 Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. Swanson R.N., Webb M.L., Strohl B Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl B Baldwin J.J., Auld D.S., "Orthologs of human receptors and methods of use."; "Orthologs of human receptors and methods of use."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF540793; AAN17319.1; -.
16.8%; Score 314.5; DB 11; Length llarity 28.1%; Pred. No. 7.7e-21; Conservative 60; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D464957687BBFEBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
16.7%; Score 313.5; DB 6;
Best Local Similarity 28.5%; Pred. No. 9.4e-21;
Matches 95; Conservative 58; Mismatches 153;
                                                                                                                                                                                                                                                                                                                 ILK-------IKGSSSSSSSST 335
                                                                                                                                                                                                                                                                                                                                                                                        355 AA.
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                 Similarity
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01-MAR-2003
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SEQUENCE
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      Query Match
                  Best Local
Matches 9
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Q8HZN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 PYHL-NIKQFWARGMLHLPSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKWL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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261 PYHLVLLTDTLMRTRLIKETCQRRNDIDRALDATEILGILHSCLNPIIYAFIGGKFRHGL 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 ACR--ARLVCVAIWTLVLLQTMPLLLLMPMTKPLVG-KLACMEYSSMESVLGLPLMVLVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AIGFCGPVGIILSCY---MKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || : : | : | || | : | || | 37 BSLEINKYFVVIIYALVFLSLIGNSLVMLVILHSRVGRSITDVYLINLAMADLLFALTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 PIWAAAKUNG--WIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHA---TRILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 PYHLVLIADTIMRTRLINETCQRRNNIDQALDATBILGILHSCLNPLIYAFIGQKFRHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 ESQIVKIFLRSLFYTALLVPSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVAL
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Bukaryota; Metazoa; Chordate; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

[1]
                                                                                                                                                                                                                                                                                                          OI-MAR-2003 (TENBELFEI: 23, Last sequence update)
01-MAR-2003 (TENBELFEI: 23, Last annotation update)
Interlenkin 8 receptor B CXCR2.
Macaca mulata (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 355;
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 16.6%; Score 310.5; DB 6; Length Similarity 28.7%; Pred. No. 1.8e-20; 95; Conservative 58; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl E Baldwin J.J., Auld D.S.; Possible Baldwin J.J., Auld D.S.; S.; Submitted (1972-2012) to the EMBL/GenBank/DDBJ databases. EMBL, AF$40792; AAN17318.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6A9BF9A921F470C5 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Interleukin 8 receptor B CXCR2.
                                                                               LGILKLKGSSSSSS----SSSSTPGKASSETPS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 LGILKLKGSSSSSS----SSSSTPGKASSET 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKILATHGLISKDSLPKDSRPSFVGSSSGHT 351
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                                                                                                                                                                                                                                                           PRT;
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37 YTALLVFSALGNILALCITCOKSRKINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AA
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PRNTNS; PR00237; GPCRAHOOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                        325 VKWLPFLSVDRLERASSTSPST 346
                                                                                                                                                                                                                                                                                                                                                     314 -KWL--LGILKLKGSSSSSSS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, CC chemokine receptor 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92; Conservative
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SEQUENCE
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Q8MJW8
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                                                                                                                                                                                                                                                                                                                                                                                          152 QKRYLVKFICLSIWGLSLLLALPVLIFRKTIYPPYVSPV-CYEDMGNNTANWRMLLRILP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 OSFGFIVPLLIMLFCYGPTLRTLFK------AHMGQKHRAMRVIFAVVLIFLLCW 259
                                                                                                                                                                                                                                                                                                                      97 PIWAASKVTG--WIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHA---TRTLT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                          FAIGFCGPVGIILSCY---MKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCF 256
                                                                                                                                                                                                                                                                                                 84 PGRVVCYVLGSSWPFGKGLCRLTAFVLYIDTYGGVYLMACVSVDHYPAVVCAHWGPRLRT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPYHL-NIKQFMARGMLHLPSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYRKW 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 LPYNLVLLADTLMRTWVIQETČERRNDIDRALEATEILGILHSCLNPLIYAFIGQKFRHG 319
                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                   Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                               24 ESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVAL
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MEDLINE=20153429; PubMed=10686294;

MEDLINE=20153429; PubMed=10686294;

A Ghannam A., Kreschmer P.J.; Pu H., Dunning L., Snider R.M.,

A Ghannam A., Kreschmer P.J.; Pu H., Dunning L., Snider R.M.,

A Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;

"Species selectivity of a small molecule antagonist for the CCR1

T. Chemokine receptor.";

I Bur. J. Pharmacol." 389:41-49(2000).

REMBL, AR127528; AA736453.1;

R. RICARDONO1; 7tm 1; 1.

R. PROSITE; PRO0021; 7tm 1; 1.

R. PROSITE; PRO0237; GPCRHODOPSN.

R. PROSITE; PRO0237; GPCRHODOPSN.

R. PROSITE; PRO0237; GPCRHODOPSN.

R. PROSITE; PRO0237; GPCRHODOPSN.
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                                                                                                                                                         16.5%; Score 309.5; DB 6; Length 355; 28.0%; Pred. No. 2.2e-20; Live 64; Mismatches 146; Indels 29.
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Best Local Similarity 27.0%; Pred. No. 2.5e-20;
Matches 87; Conservative 61; Mismatches 132; Indels
40928 MW; 2B01C47E9874A2C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chemokine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGILKLKGSSSSSS----SSSSTPGKASSET 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLKILAIHGLISKDSLPKDSRPSFVGSSSGHT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 AA
                                                                                                                                                                                            93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
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                                                                                                                                                         Query Match
                                                                                                                                                                               Local
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Q9MYJ8
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268
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                                                                                                                                          100 VFGNAMCKVLSGFYYTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIIIWV 159
                                                                                                                                                                                                                    157 LVLLQTMPLLLMPMTKPLVGKLACMEYSSMES-----VLGLPLMVLVAFAIGFCGPV 208
                                                                                                                                                                                                                                                                                                                                                                    213 LVMIVCYTGIIKILLRRPNE----KKSKAVR---LIFVIMIIFFLFWTPYNLTLISVF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 QDFLFTYGCEQGRQLDLAIQVTEMIAYTHCCVNPVIYAFVGERFRKHLRQLFHRRVAVHL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Maeda S., Okayama T., Masuda K., Ohno K., Tsujimoto H.;
"Detection of CC chemokine receptor 4 (CCR4) mRNA expression in canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 PLGTMLFCYSMIIRTLQHCKNEKKSK------AVRMVFAVVALFLGFWAPY-
                             41 YSLVEVIGLYGVILVVVVJVQYKRLKAMTSIYLLNLAISDLLFLFTLP-FWISYQLKTDW
                                                                                                          97 PFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWT
                                                                                                                                                                                                                                                       209 GIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKOFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 VVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRTAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 ---YYAADQWVFGLGLCKIISWMYLVGFYSGIFFIMLMSIDRYLAIVHAVFSLRARTLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 ARLVCVAIWTLVILQTMPLLLMPMTXPLVGKLACMEYSSMESVLGLPLMVLVAFAIGFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PVGIILSCYMKI--TWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAVVVCF----SPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 KIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVALP--GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 ELFLPPL-YSLVFLFGLLGNSVVVVVLFYXKRLKSMTDVYLLNLAISDLLFVLSLPFWG-
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Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                           269 RGMLHLPSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTHYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.4%; Score 308.5; DB 6; Length 360; 27.8%; Pred. No. 2.8e-20; ative 59; Mismatches 135; Indels 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atopic skin lesion.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB080188; BAC10546.1; -.
InterPro; IFR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl B., Baldwin J.J., Auld D.S.; Cythologs of human receptors and methods of use."; Submitted (MIC 2002) to the EMBL/GenBank/DDBJ databases. EMBL, AF540789; AAN17315.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Testis;
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                                                                        SEQUENCE
                                                                                              Query Match
                                                                                                            Best Local
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Matches
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Q8NE10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLVAPAIGFCGPVGIILSCY---MKITWKLCSTAREDPVTSRKGRHWRGCLLTLLMLVAV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 RILPQSFGFIVPLLIMLFCYGFTLRTLFK------AHMGQKHRAMRVIFAVVLIF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 VVCFSPYHL-NIKQFMARGMLHLPSCAERRAFLLSLQATVALMNMNCGITPIIYFFASTH 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIKOFMAR--GMLHIPSCAERRAFILSLOATVALMMNCGITPIIYFFASTHYRKWILG 318
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                                                                                                                                                                                                                                                                                                                                                                                                   24 ESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSRKINCTGIYLVHLAVSDLLFTVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Interleukin 8 receptor B CXCR2.
Par troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhin; Hominidae, Pan.
                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                      16.3%; Score 306.5; DB 4; Length 355; 28.0%; Pred. No. 4.2e-20; cive 61; Mismatches 144; Indels 37
                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037961; AAH37961.1; -.
                                                                                                                                                                                                                                                                                                                                355 AA; 40122 MW; 809AB63ADA6A42C6 CRC64;
                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                    LKGSSSSSSSST 335
                                                                        318 LFKTCRGPFMLCOYCRLLOMYSPDTPSSSYT 348
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                                                                                                                                                                                            Interleukin 8 receptor, beta.
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Best Local Similarity 2000.
Best Local Similarity
Conservative
The 94; Conservative
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SEQUENCE FROM N.A.
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TISSUE=Brain;
                                                      319 ILK----
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                                                                                                                                                                                                                                       NCBI TaxID=9606;
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Q8HZN8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 NMPNKSVLLYTLSFIYIFFVIGMIANSVVWWNIQAKTTGYDTHCYILNLAIADLWVVL
                                                                                                                                                                                                                                                                                                                                      144 AGR--ARLVCVAIWTLVTLQTMPLLLMPMT-----KPLVGKLACMEYSSMESVLGLPLM
                                                                                                                                                                                                                                                                                                                                                                       196 VLVAFAIGECGPVGIILSCY---MKITWKLCSTAREDPVTSRKGRHWRGCLLITLLMLVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 RILPQSFGFIVPLLIMLFCYGFTLRTLFK------AHMGOKHRAMRVIFAVVLIF
                                                                                                                                                                                                                                       84 PGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYLMACVSVDHYPAVVCAHWGPRLRT
                                                                                                                                                                                                                                                                   97 PIWAASKUNG--WIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHA---TRTLT
                                                                                                                                                                         ESQTVKI FLRSLFYTALLVFSALGNI LALCLTCQKSRKINCTGI YLVHLAVSDLLFTVAL
                                                                                                 Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                              th 16.3%; Score 306.5; DB 6; Length Similarity 28.0%; Pred. No. 4.2e-20; 94; Conservative 61; Mismatches 144; Indels
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Strausberg R.;
Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.,
EMBL; BCO66661, AAH36661.1;
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
HYPOthetical protein.
HYPOthetical protein.
SEQUENCE 362 AA; 41478 MM; BOCOECIABSFBIFBB CRC64;
355 AA; 40122 MW; 809AB63ADA6A42C6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 YRKWLLGILKLKGSSSSSS----SSSSTPGKASSET 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Job time : 43 secs

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253 VVCFSPYHLNIKQFMARGMLHLPSCAERRAFLLSLQATVALMMNCGITPIIYFFASTHY 312
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                                                                                                                                                                                                                                                                                                                                                                                                  265 WLPYHVAVLLDIFSILHYIPFTCRLEHALFTALHVTQCLSLVHCCVNPVLXSFINRNYRY 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 PLRIY-YYINRHWPFQRALCLICFYLKYLNMYASIFFLTCISLQRCLFLLKPFRARNWKR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 RIRTAGRARIVCVAIWTLVTLQTMPLLIMPMTKPLVGKLAC----MEYSSMESVLGLPL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 IVCFTPYHLNFPFFMVXQRVFSNCSFIRNTLCFHISLCLANINCCLDPVVYYFMISEF 301
                                                                RTAGRARLYCVAIWTLVLLQTMP--LLLMPMTKPLVGKLACM----EYSSMESVLGLPLM 195
                                                                                                             196 VLVAPAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWRGCLLTLIMLVAVVVC 255
                                                                                                                                                                                                                                                          213 ELVSVVLGFAVPFSIVAVFYFLLARAISASSDQEXHSSRK------IIFSXVVVFLVC 264
                                                                                                                                                                                                                                                                                                                                                         256 FSPYHLNIKQFMARGMLHLP-SCAERRAFLLSLQATVALMNMUCGITPIIYFFASTHYRK 314
96 TIPVWVVSLVQHNQWPMGELTCKVTHLIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYLTFQYSLYATTYIFIFIFGLLANSVALWYLCRFISKKNKAIIFMINLSVADLAHVLSL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Mature 420:563-573(2002).
EMBL: AKO41140; BAC31049.1; -.
SEQUENCE 352 AA; 40382 MW; C9977E40202AB4EA CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to putative purinergic receptor P2Y10.
Mus musculus (Mouse)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 WLL-----GILKLKGSSSSSSSS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 ELMKAFIFKYSAKTGLTKLIDASRVSETEYS 355
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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Best Local Similarity 27.94
Matches 84; Conservative
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098Y68
AC Q8BY68
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Search completed: February 19, 2004, 19:34:23

Human liver peptid Peptide #10559 enc Protein #8223 enco

Human ORFX protein Human novel secret Human novel polype Human brain express Human bone marrow Peptide #10319 enc Human peptide enco Human novel polype Novel human secret Human polypeptide Human polypeptide Novel human secret C glutamicum prote Drosophila melanog Human diagnos Novel human diagno Novel human diagno Novel human diagno Novel human diagno Novel human diagno Novel human diagno Novel human diagno Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

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G protein coupled receptor related protein; human, GPCR, cardiomyopathy; atherosclerosis, diabetes; cancer; stroke; von Hippel-Lindau syndrome; Alzheimer; disease; tuberous sclerosis; hypercalcaemia; Parkinson's disease; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; addiction; anxiety; depression; paln; obesity; Crohn's disease; infertility; hypertension; scleroderma; arthmitis; human immunodeficiency virus; autoimmune disease; HIV;
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                    ABG58455
ABB43053
ABB26224
                                                                                                                  AAU32634
AAG91288
                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; graft-versus-host disease.
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                                          AAM63955
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                                                               AAM36882
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                                                                                                                                ABB6919
                                                                                                                                                                                                                                                                                                                     ABG32286 standard; Protein; 360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2001; 2001US-259552P.
09-JAN-2001; 2001US-260544P.
20-MAR-2001; 2001US-277405P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002; 2002WO-US00056
(first entry)
                                                                                                                                                                                                                                                                                                                                                                Human GPCR16 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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RESULT 1
ABG32286
Drosophila melanog
Novel human secret
Drosophila melanog
Novel human secret
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Human novel polype
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Human G protein-co
Human G Protein-Co
                                                  2004, 19:33:35; Search time 43 Seconds (without alignments) (without alignments) 1328.874 Million cell updates/sec
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       . GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                1107863 seqs, 158726573 residues
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ABG66698
ABG14682
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AAU25588
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AAU32705
                                     protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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360
1 MIKLGPYFTPPTKI)
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360 86 86 70 70 112 112 112

Score

Result No.

Human polypeptide Human novel secret Human novel polype Cryptosporidium

Human

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(CURA-) CURAGEN CORP.
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Kekuda R; Smithson G, Ellerman K, Edinger SR, Muralidhara P; Casman SJ,

2002-643487/69. N-PSDB; ABS64723 New isolated G protein coupled receptor polypeptides and polynucleotides, useful in gene therapy, particularly for treating preventing cardiomyopathy, atherosclerosis, diabetes, multiple polynucleotides, useful in gene therapy preventing cardiomyopathy, atherosclero sclerosis, Crohn's disease or cancer

Claim 1, Page 98; 252pp; English.

This invention relates to a new isolated G-protein coupled receptor

(GPCRX) polypeptide, GPCRX nucleic acid and an antibody specific to the protein

are useful of GPCRX nucleic acid and an antibody specific to the protein

are useful for treating, preventing or alleviating a GPCRX-associated

disorder or a pathological state in a subject, particularly a human. In

particular, the disorder is cardiomyopathy, atherosolerosis, diabetes,

or a disorder related to cell signal processing and metabolic pathway

or adisorder related to cell signal processing and metabolic pathway

or adisorder related to cell signal processing and metabolic pathway

or adisorder related for predisposition to a disease associated

with altered levels of GPCRX, particularly cancer. The GPCRX nucleic

disponsing the presence of or predisposition to a disease associated

with altered levels of GPCRX, particularly cancer. The GPCRX nucleic

considerament for therapeutic or prophylactic applications for disorders

associated with aberrant GPCRX expression or activity, e.g. von

Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous

considerated with aberrant GPCRX expression or activity, e.g. von

Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous

considerated with aberrant GPCRX expression, attain-index of disease,

constant the pale of a level of the procession or activity, bowel

constant the pale of the procession or activity, and alsease,

constant the pale of the procession or activity, and and activity attain, and and and activity hypertension, coleroderma, inamposing the procession

constant the pale of produce antibodies and as vaccines. The mucleic acids are improved in sease. The DNA encoding the procession or produce antibodies and as vaccines. The mucleic acids are further used as hybridiation probes, in chromosome mapping, tissue

constant disease. The DNA encoding the procession or the present of in developing powerful as and pharmacogenomics. These are also useful

indexident the procession or activity or human disorders, as well as in diagnostic applications. The present sequence represents a human G protein coupled receptor related protein sequence represents a hu (GPCR) of the invention. represents a

360 AA; Sequence

ö ò DB 23; Length 360; 0; Indels 100.0%; Score 360; I 100.0%; Pred. No. 0; cive 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 360; Conservative

1 MIKLGPYFTPPTKIKTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR 60 1 MIKLGPYFTPPTKIKTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR

61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVXL 120

121 MACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQIMPLLLMBWTKPLVGKLAC 180 181 MEYSSMESVLGLPLMVLVAFAIGFCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR

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GCLITILMIVAVVVCESPYHLNIKQFMARGMLHLPSCAERRAFLLSLQATVALMNMNCGI 300 GCLLTLIMIVAVVVCFSPYHLNIKQFMARGMIHLPSCAERRAFLLSLQATVALMNMVGI 300 241

181 MEYSSMESVLGLPLMVLVAPAIGPCGPVGIILSCYMKITWKLCSTAREDPVTSRKGRHWR 240

301 TPIIYFFASTHYRKWILGILKIKGSSSSSSSSSTPGKASSETPSITQARGSMFLAEHVV 360 301 TPIIYFFASTHYRKWILGILKIKGSSSSSSSSSTPGKASSETPSITQARGSMFLAEHVV 360 ò

RESULT 2 **AB**G66698

ABG66698 standard; Protein; 110 AA

ABG66698;

(first entry) 30-AUG-2002

Human novel polypeptide #33.

Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; hematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelat disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; home degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; fungal infection

sapiens.

WO200244340-A2

06-JUN-2002.

30-NOV-2001; 2001WO-US47004.

30-NOV-2000; 2000US-0028952.

HYSE-) HYSEQ INC

à Wang Wang J, Asundi V, Liu C, Zhou P, Drmanac RT; Goodrich RW, 7, Ujwal ML, famazaki V, Tang

WPI; 2002-508509/54. N-PSDB; ABK94922.

Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -

Claim 10; Page 600; 672pp; English.

The invention relates to human novel polymucleotides and associated correct the invention relates to human novel polymucleotides are useful for treating inflammatory conditions such as arthritis, mebhritis, Crohn's disease, ischaemia-reperfusion injury, abock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and contains and are useful for the treatment of central and partipheral nearous system diseases and neuropathies, such as Alzheimer's disease, Dazin tissue, The sequences are involved in chemotactic or chemokinetic sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of hazantopolesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, regeneration of bone, carrilage, tendon, ligament and/or nerve tissue contains, sequences of the invention are also useful for gut disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or librosis. Creperfusion injury in various tissues, immune deficiencies and disorders infections, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human converse.

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at ftp.wipo.int/pub/published_pct_sequences
                                                 Sequence
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Matches
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Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                              141 LRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAF 200
                                                                                                                                                                                21 LRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAF 80
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
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                                                 Length 110;
                                                                                             0; Indels
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                                                 DB 23; L
                                            Query Match
23.9%; Score 86; DB
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 86; Conservative 0; Mismatches
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                                                                                                                                                                                                                                               201 AIGECGPVGIILSCYMKITWKLCSTA 226
                                                                                                                                                                                                                                                                              81 AIGFCGPVGIILSCYMKITWKLCSTA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #14673.
                                                                                                                                                                                                                                                                                                                                                                                                                  ABG14682 standard; Protein; 377 AA
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
N-PSDB; AAS78869.
110 AA;
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  Sequence
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AAG14682
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                                                                                                                          141 LRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSMESVLGLPLMVLVAF
                                                                                                                                                                             116 LRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKCACMEYSSMESVLGLPLMVLVAF
                                                                    Gaps
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                 Length 377;
                                                                    Indels
              DB 22; L
8.8e-75;
23.9%; Scor.
100.0%; Pred. No. o...
'... 0; Mismatches
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                                                                                                                                                                                                                                         201 AIGFCGPVGIILSCYMKITWKLCSTA 226
                                                                                                                                                                                                                                                                          176 AIGFCGPVGIILSCYMKITWKLCSTA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU19222 standard; Protein; 177 AA
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08-MAR-2000; 2000US-0187828.

08-MAR-2000; 2000US-0187829.

08-MAR-2000; 2000US-0187830.

08-MAR-2000; 2000US-0187831.
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08-MAR-2000; 2000US-0189294.
08-MAR-2000; 2000US-0187929.
08-MAR-2000; 2000US-0187928.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                         Local Similarity 100.
nes 86; Conservative
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51;
                                                                     Vogeli G,
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Best Local
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                  The invention relates to novel isolated nucleic acid molecules encoding G protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides, C polyapeptides, and modulators may be used in the transment of diseases and conditions such as infections, much as viral infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, annexis, hypotension, hypotension, myocardial infarction, and cardioratial disorders, including schizophrenia, migraine, major neurological disorders, including schizophrenia, migraine, major cherosclerosis, such as Huntington's disease or Tourette's Syndrome dyskinesias, such as Huntington's disease or Tourette's Syndrome condulators, may other diseases and syndromes listed in the specification.

C and many other diseases and syndromes listed in the specification.

C noptors, may also be used in diagnostic assays for such diseases or and antity of the invention sequence represents a G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, G-protein coupled receptor; GPCR; mental disorder; schizophrenia; attention deficit disorder; anxiety, depression; bipolar disorder; neurological disorder; Huntington's disease; dementia; obseity; anorexia; metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis; type 2 diabetes; cardiovascular disorder; myocardial infarction; cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
                                                                                                                                                                                                                                                                                                              233 SRKGRHWRGCLLTLLMLVAVVVCFSPYHLNIKQFWARGMLHLPSCAERRAFLLSLQATVA 292
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                           Query March
19.4%; Score 70; DB 22; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 70; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G Protein-Coupled Receptor (GPCR) polypeptide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antidepressant; anorectic; gene therapy
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 Claim 31; Page 281; 336pp; English
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2000US-0184304.
2000US-0184305.
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2000US-0188880.
2000US-0194344.
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2000US-0217369
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000US-0186457
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                                                                                                                                                                                                               receptor of the invention.
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                                                                                                                                                                                                                                       Sequence 177 AA;
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Sequences AAU25554-AAU25616 represent human G-protein coupled receptor. (GPCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, a GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as huntington's disease and Tourette's syndrome, metabolic disorders such as obesity, anorexia and type 2 diabetes, cardiomyopathy and atherosclerosis, wiral infections caused by HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 LRTAGRARLYCVAIWTLVLLQTMPLLLMPMTKPLVGKLACMEYSSNESVLG 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 35; Page 83; 279pp; English.
                                                                                                                                                                                    Wood LS, Parodi LA,
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                                                                                                                           (PHAA ) PHARMACIA & UPJOHN CO
11-JUL-2000; 2000US-0217370.
14-JUL-2000; 2000US-0218337.
20-JUL-2000; 2000US-0218492.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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N-PSDB; ABL11956.
                                                                                                                                                                                                                                                   MPI; 2001-570628/64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 AA;
                                                                                                                                                                                                                                                                                     N-PSDB; AAS42840.
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The invention relates to novel human secreted polypeptides. The polypeptides are useful for polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying atterapeutic agent for use in treatment of a pathology related to aberrant expression or
                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention signatorics genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration; immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                 Disclosure; SEQ ID NO 30351; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 13; DB 22; Length 311; 00.0%; Pred. No. 0.00062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein #3140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU32649 standard; Protein; 106 AA
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26-JAN-2001; 2001US-0770160.
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nes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                 311 AA;
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                                                  interactions
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                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.—cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furugs. The invention discloses, consequences (ABL1615-ABL30511), expressed DNA sequences (ABL16175-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence data for this patent did not form part of the printed scification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and thereby, and can be used as nutritional supplements. They may be used tincrease stem cell proliferation; to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias AAUS9510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                       3.3%; Score 12; DB 22; Length 106;
100.0%; Pred. No. 0.0021;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 39309.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                         KGSSSSSSSS 334
                                                                                                                                                                                                                                            Local Similarity 100.
Les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
N-PSDB; ABL14942.
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                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                          106 AA;
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                          Query Match
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therapy -
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Human, open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease, diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

myasthenia gravis.

WO200192523-A2 Homo sapiens.

06-DEC-2001.

Human ORFX protein sequence SEQ ID NO:21886.

(first entry)

24-JUN-2002

ABP1:0952;

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ABP10952 standard; Protein; 86

RESULT 10 ABP10952

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to increase stem cell prodiferation, to reginate the proteins of the polypeptides and cells genetically confineered to express them are also useful for producing the proteins. They may be used to increase stem cell prodiferation, to reginate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; impure suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                  Human, vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopolesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemla.
                                     Gaps
                                   ö
3.3%; Score 12; DB 22; Length 1262; 00.0%; Pred. No. 0.022; ve 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 652; 765pp; English.
                                                                                                                                                                                                                                                                                                                    Novel human secreted protein #3196
                                                                                                                                                                                                        AAU32705 standard; Protein; 85 AA
       100.08; FIT
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26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                                                (first entry)
                                                                         324 GSSSSSSSST 335
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                                     Conservative
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                 Best Local Similarity
Matches 12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200179449-A2.
                                                                                                                                                                                                                                                                                18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens,
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                                     12;
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                                                                                                                                                                                                                                              AAU32705;
     Query Match
                                                                                                                                                                       RESULT 9
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30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P. 29-MAY-2001; 2001WO-US10836.

Shimkets RA, Leach MD; (CURA-) CURAGEN CORP.

API; 2002-106308/14.

N-PSDB; ABN26704.

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27522 encode the human ORFX proteins are useful for in the specification approach of the manufacture of a medicament for treating a creating a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide capturence can be used in gene therapy. ORFX sequences can be used in the therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumnours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders, infectious disease, autoimmune disorders such as multiple sclerois, rheumatoid arching, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, incisions, ulcers, for treating osteoporosis, conceptuation or regeneration and treatment of lung or liver fibrosis, mystemic cytokine damage.

Consequence of lung or liver fibrosis, when the printer of lung or liver fibrosis, when the comment of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the printer of the print
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DB 23;

3.1%; Score 11;

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Gaps

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Best Local Similarity 100. Matches 11, Conservative

Query Match

324 GSSSSSSSS 334

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GSSSSSSSSS

42

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders

Disclosure; SEQ ID 21886; 1037pp; English.

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011-8887-2000;
01-8887-2000;
05-8887-2000;
06-8887-2000;
06-8887-2000;
06-8887-2000;
08-887-2000;
08-887-2000;
08-887-2000;
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08-887-2000;
08-887-2000;
08-887-2000;
                                                                                                    12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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                                                                                                                              Human; immunosuppressive; antiarthritic; antirheumatic; cardiant; vasotropic; cerebroprotective; nootropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral isohaemia; angiogenesis; nerevous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
         Gaps
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Pred. No. 0.016; i Mismatches 0; Indels
                                                                                                                 Human novel secreted protein, Seq ID 1273.
                                                                     AAU16320 standard, Protein, 94 AA.
Best Local Similarity 100.0%; Pr
Matches 11; Conservative 0;
                                                                                                                                                                                                                                                              31-JAN-2000, 2000US-0179065.
24-FEB-2000, 2000US-0180628.
22-FEB-2000, 2000US-0184664.
02-MAR-2000, 2000US-018974.
17-MAR-2000, 2000US-0190076.
18-AFR-2000, 2000US-0190076.
19-AFR-2000, 2000US-020515.
07-JUN-2000, 2000US-0205467.
28-JUN-2000, 2000US-0205467.
                                                                                                                                                                                                                                                 17-JAN-2001; 2001WO-US01341
                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0225268
                                                                                                   07-NOV-2001 (first entry)
                     324 GSSSSSSSSS 334
                                  27 GSSSSSSSSS 37
                                                                                                                                                                                                                     WO200155322-A2.
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14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
18-AUG-2000)
22-AUG-2000)
22-AUG-2000)
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                                                                                     AAU16320;
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(first entry)

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Human; neural disorder; immune system disorder; renal disorder; muscular disorder; disease; reproductive disorder; perspiratory disease; reproductive disorder; pagastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; annex; immunosuppressive; antinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                      ABU55389 standard; Protein; 94 AA.
                                                                                                                 Human novel polypeptide #476.
                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                        18-MAR-2003
                                                               ABU55389;
                                                 The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliotate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune disease e.g. rheumatoid arthritis, include autoimmune disease e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebral adsorders e.g. cardiac arrest, cerebral adsorders e.g. cardiac arrest, cerebral disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other of prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preventive to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other mutritional components. The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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100.0%; Pred. No. 0.018;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM;
                                   2000US-0249216.
2000US-0249217.
2000US-0249218.
2000US-0249244.
2000US-0249245.
                                                                                                                 2000US-0249265.
2000US-0249297.
2000US-0249299.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                           17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                 DEC-2000;
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000US-229287P.
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                                                  17-JAN-2001; 2001US-0764864
US2002132753-A1
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                                                                            31-JAN-2000;
                                                                                          04-FEB-2000;
28-JUN-2000;
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                          19-SEP-2002
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22-AUG-20
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Gaps ö

324 GSSSSSSSSS 334

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03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
7-SEP-2000; 2000US-023559.
04-OCT-2000; 2000GB-0024263.
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21-SEP-2000;
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                                                                                Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for traating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and simusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperprofilerative disorders (e.g. Hoddxin's disease and leukaemia), inflammatory diseases (e.g. conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases.

Sequences ABUSSA914-ABUSSA99 and ABUSS748 represent human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                           New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.1%; Score 11; DB 24; Length 94;
100.0%; Pred. No. 0.018;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  Claim 11; SEQ ID NO 1273; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human liver peptide, SEQ ID No 37103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG58455 standard; Peptide; 104 AA.
                                                                                                    Rosen CA, Ruben SM, Barash SC;
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2000US-0207456.
2000US-0608408.
17-NOV-2000; 2000US-249299P.

08-DEC-2000; 2000US-251856P.

08-DEC-2000; 2000US-251869P.

08-DEC-2000; 2000US-251869P.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                        WPI; 2003-147444/14.
N-PSDB; ABX73648.
                                                      (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       94 AA;
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26-MAY-2000; 2
30-JUN-2000; 2
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Note: The sequence information for this patent does not appear in the printed specification but, was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                 probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1%; Score 11; DB 22; Length 104; Best Local Similarity 100.0%; Pred. No. 0.02; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published pct sequences.
                                                                                                                                                                                                 Human genome-derived single exon nucleic acid analysing gene expression in human adult liver
                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 37103; 658pp; English
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                                                                 Chen W, Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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                                                                 Hanzel DK,
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Protein #8223 encoded by probe for measuring heart cell gene expression.
                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart ABA21535-ABA41305). The present sequence is a protein encoded by one
                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                         Claim 27; SEQ ID NO 35688; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                  3.1%; Score 11; 'DB 22; Length 104; 100.0%; Pred. No. 0.02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB26224 standard; Protein; 104 AA.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
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probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardidac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at tp.wipo.int/pub/published_pct_sequences.
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ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 11; Conservative
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Search completed: February 19, 2004, 19:37:18 Job time : 44 secs

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Gaps

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NAME: CSET, LUARN
REGISTRATION WUMBER: 31,825
REPERENCE/DOCKET NUMBER: GI 5:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)876-1170
TELEFAX: (617)876-1170
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: AMINO ACID
                    02140
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Sequence 5812, Ap
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Sequence 30, Appl
                                                                                                                        February 19, 2004, 19:36:26 ; Search time 21 Seconds (without alignments) 725.329 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 30,
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/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-07-757-022B-90

US-07-757-022B-92

US-07-757-022B-94

US-07-757-022B-94

US-07-757-022B-76

US-07-757-022B-76

US-07-757-022B-70

US-07-757-022B-70

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US-08-61-136C-22

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US-07-757-022B-104
US-07-757-022B-142
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                                                                                                                                                                                                                                                                                                                                                          328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                              OLIGO
Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                        Sequence:
                                                                                                                          Run on:
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US-07-757-0228-62
US-08-030-822A-90
US-09-101-156A-39
US-09-101-156A-39
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US-09-101-156A-39
US-09-001-156A-39
US-09-001-156A-39
US-09-001-156A-39
US-09-001-156B-39
US-09-001-1793A-39
US-09-001-1793A-39
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US-09-001-178-9
US-09-001-178-9
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148
221
222
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349
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Threat Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STREET: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC Compatible
COMPUTER: ELBM PC Compatible
COMPUTER: DEAD PC COMPOSIMS.
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/643,502
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTONEY/AGENT INFORMATION:
ANAME: CANADATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: US AUG-1989
ATTONEY/AGENT INFORMATION:
ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME: ANAME
Sequence 12, Application US/07757022B Patent No. 6433142
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168 SSSSSSSST 178
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 204 amino aci
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US-07-75-022B

Patento No. 6433Latton US/07757022B

Patento No. 6433Latton

APPLICANT: Gener. Thomas G

APPLICANT: Clark. Stephen C

APPLICANT: Gener. Retherine

APPLICANT: Haw-tck, Rodney W.

TITLE OF INVANITON: Negakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

ADDRESSER: Genetics Institute, Inc.

STREET: 87 Cambridge-Park Drive

CITY: Cambridge-Park Drive

CITY: Cambridge-Park Drive

COUNTRY: 13.6.A.

ZIP: 0124 Massachusetts

COUNTRY: 13.6.A.

ZIP: 0124 Massachusetts

COMPUTER: RADABLE FORM:

WEDIOM TYPE: Floppy disk

COMPUTER: 130

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                                                                                                                                    3.1%; Score 11; DB 4; Length 43; 100.0%; Pred. No. 0.0038; tive 0; Mismatches 0; Indels
                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                             325 SSSSSSSST 335
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-757-022B-12
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1 Sequence 22, Application US/0775022B

1 Sequence 22, Application US/0775022B

1 Sequence 22, Application US/0775022B

1 Sequence 22, Application US/0775022B

2 Sequence 22, Application US/0775022B

2 APLICANT CLARK, Stephen C.

3 APLICANT CLARK, Stephen C.

4 APLICANT CLARK, Stephen C.

5 APLICANT CLARK, Stephen C.

5 APLICANT CLARK, Stephen C.

5 APLICANT CLARK, STEPHEN C.

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: 209 amino acids
AMINO ACID
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-757-022B-94
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Pred. No. 0.016;
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Patent No. 6433142

GENERAL INFORMATION:
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hawick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCES: 143
CORRESPONDENCES: 161
STATE: ADDRESSEE: Genetics Institute, Inc.
STATE: Massachusetts
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                              COMPUTER: NOISE

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/57,022B
FILING DATE: 18-JAN-1991
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 29-JDC-1969
FILING DATE: 29-DEC-1969
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1969
ATTORNEY/AGENT INFORMATION:
NAME: CSert, Luarn
REGISTRATION NUMBER: 31,822
REBRERENCE/MONICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.1%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 132: SEQUENCE CHARACTERISTICS: LENGTH: 208 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 SSSSSSSST 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-07-757-0228-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-07-757-022B-94
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Sequence 76, Application US/07757022B

Sequence 76, Application US/07757022B

Patent No. 643342

GENERAL INFORMATION:

APPLICANT: Clerk, Stephen C.

APPLICANT: Turner, Katherine

APPLICANT: Turner, Katherine

APPLICANT: Hewick, Rodney M.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STREET: Massachusetts

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11, DB 4; Length 209; Pred. No. 0.016; 0; Mismatches 0; Indels
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/643,502
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/390,901
FILING DATE: 29-DEC-1989
ATFORNEY/AGENT INPORMATION:
APPLICATION NUMBER: 31,822
FILING DATE: 08-AUG-1989
ATFORNEY/AGENT INPORMATION:
TELEPHONE (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: CAPARACTERISTICS:
TELEPATION CONTACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
FILING DATE: 19910910
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APPLICANT: Gener, Thomas G.
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Thurer, Katherine
APPLICANT: Hawick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
GITY: Cambridge Institute, Inc.
GITY: Massachusetts
COUNTRY: U.S.A.
ZIP: OZ140
COMPUTER: Replable FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 18-JOH 1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
FILING DATE: 39-DEC-1989
FILING DATE: 39-DEC-1989
FILING DATE: 39-DEC-1989
FILING DATE: 39-DEC-1989
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FILING DATE: 39-DEC-1989
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FILING DATE: 39-DEC-1989
FILING DATE: 39-DEC-1989
FILING DATE: 39-DEC-1989
FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 220;
                        ATTORNEY AGENT INFORMATION:
NAME: Ceerr. Luam.
RAGISTRATION WUBER: 31,822
REGISTRATION WUBER: 31,822
REFRENCE/DOCKET WUBER: GI 5190
TELEPOMPUNICATION INFORMATION:
TELEPOMPUNICATION SEQ ID NO: 96:
SEQUENCE GIARACTERISTICS:
LENGTH: 220 amino acids
       US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
3.1%; Scc
Best Local Similarity 100.0%; P;
Matches 11; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                       : 220 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 SSSSSSSST 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 SSSSSSSSST 178
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-0228-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-757-022B-30
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: CambridgePark Drive
CUTY: CambridgePark Drive
COUNTRY: U.S.A.
COMPUTER: Flopy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION NUMBER: US/07/757,022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11; DB 4; Length 217; Pred. No. 0.017; 0; Mismatches 0; Indels
                                                 PRICEALCATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: US 07/390,901
FILING DATE: US 07/390,901
FILING DATE: US 07/390,901
FILING DATE: US NUMBER: US 07/390,901
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)876-1170
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)876-1170
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)876-1170
TELECOMMUNICATION OF:
SEQUENCE CHARACTER:STICS:
LENGTH: 217 amino acids
TYPE: Amino Acids
TYPE: Amino Acids
TYPE: Amino Acids
TYPE: Amino Acids
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APPLICATION WUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-757-022B-96; Sequence 96, Application US/07757022B; Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.1
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 SSSSSSSST 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-07-757-0228-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
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PATENT NO. 6001639
GENERAL INFORMATION:
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Lange. Lene N.
APPLICANT: Lange, Lene Markus S.
APPLICANT: Lange, Lene Markus S.
APPLICANT: Inara, Michiko
APPLICANT: Takagi, Shinobu
TITLE OF INVENTION: No. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60016390 No. 6001639disk of No. 6001639th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
COUNTRY: United States of America
STREET: New York
COUNTRY: United States of America
STREET: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRESTRICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICANT: APPLICATION NATA:
APPLICANT: APPLICATION NATA:
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APPLICANT: APPLICATION NATA:
APPLICANT: APPLICATION NATA:
APPLICANT: APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 11; DB 3;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%; bcc. No. c. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-229-911A-22
Sequence 22, Application US/09229911A
Patent No. 6387690
Patent No. 6387690;
ABRICANT: Schulein, Martin
Applicant: Schulein, Martin
Andersen, Lene N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lassen, Soren F.
Kauppinen, Markus S.
                                                                                                                                                                                                                                Sequence 22, Application US/08651136C Patent No. 6001639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGIESTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lange, Lene
Nielsen, Ruby I.
Ihara, Michiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-89555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.1
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 SSSSSSSSST 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 SSSSSSSST 335
                          325 SSSSSSSST 335
                                                                                    168 SSSSSSSST 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-651-136C-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                RESULT 10
US-08-651-136C-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                                                                                                                                          Score 11; DB 4; Length 231;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70, Application US/07757022B
| Sequence 70, Application US/07757022B
| Patent No. 643142|
| GENERAL INFORMATION:
| APPLICANT: Clark, Stephen C. | APPLICANT: Clark, Stephen C. | APPLICANT: Turner, Katherine | APPLICANT: Hewick, Rodney M. | TITLE OF INVENTION: Megakaryocyte Stimulating Factors | NUMBER OF SEQUENCES: 143 | CORRESPONDENCE ADDRESS: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FLOAD disk
MEDIUM TYPE: Floapy disk
MEDIUM TYPE: Floapy disk
COMPOTER: IEM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 330
CRIASSIFICATION NUMBER: US 07/643,502
PRICK APPLICATION NUMBER: US 07/643,502
PRICK APPLICATION NUMBER: US 07/646,114
FILING DATE: 18-JAN-1991
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 18-DEC-1989
FILING DATE: 18-DEC-1989
FILING DATE: 18-DEC-1989
FILING DATE: US 07/390,901
FILING DATE: US DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: US DATA:
APPLICATION NUMBER: 31,822
NAME: CSELY, LUMIN
REGISTRATION NUMBER: 31,822
PREPERBANCE/DOCKET NUMBER: 31,822
                                                                                                                                                                                                          Query Match 3.1%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                          LENGTH: 231 amino acids
FYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-0228-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADLALL
STREET: 87 CMC
CITY: Cambridge
TMM: Massachusetts
SEQUENCE CHARACTERISTICS LENGTH: 231 amino acid
                                                                                                                                                                                                                                                                                                                                     325 SSSSSSSST 335
                                                                                                                                                                                                                                                                                                                                                                                             168 SSSSSSSST 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-07-757-022B-70
                                                                                                                                                                                                                                                                                                                                         8
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us-10-041-615-34.oli10.rai

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Score 11, DB 4, Length 372;
Pred. No. 0.027;
0, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 68, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Turner, Ketherine
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: ADDRESSEE: Generics Inc.
STREET: 87 CambridgePark Drive
CITY: CambridgePark Drive
CITY: Cambridge
STATE: Wassachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER: BAD PO Compatible
COMPUTER: END PO Compatible
COMPUTER: Ploppy disk
COMPUTER: Par POCDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-70M-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UWN-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
CLASSIFICATION: 530

REIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
FRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
FILING DATE: US 07/390,901
FILING DATE: US 07/390,901
FILING DATE: US 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                      NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I: 372 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 SSSSSSSST 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-07-757-022B-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-757-022B-64
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                                                                                    ADDRESSEE: No. 63876900 No. 6387690disk of No. 6387690th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                       3.1%; Score 11; DB 4; Length 310; 100.0%; Pred. No. 0.023; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megkaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Generics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Wassachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ins PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
       Takagi, Shinobu
TITLE OF INVENTION: No. 6387690el Endoglucanases
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-229-911A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/07757022B
Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 SSSSSSSST 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-757-022B-64
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3.1%; Score 11; DB 4; Length 463; 100.0%; Pred. No. 0.033;
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Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: ADDRESSEE: Generics institute, Inc.
STREET: 87 CambridgePark Drive
CITY: CambridgePark Drive
CITY: Cambridge
STATE: 102140
CONFUTEY: U.S.A.
ZIF: 02140
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Tal PR PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-040-1991
FILING DATE: 18-040-1991
FILING DATE: 29-040-1990
FILING DATE: 29-040-1990
FILING DATE: 29-040-1990
FILING DATE: 18-040-1990
FILING DATE: 18-040-1990
FILING DATE: 19-040-1990
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FILING DATE: 19-040-1990
FILING DATE: 19-040-1990
FILING DATE: 19-040-1990
FILING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 676-5851 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                    : 423 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                              325 SSSSSSSST 335
                                                                                                                                                                                                                                                                                                                                                                                                                        128 SSSSSSSST 138
            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 423 amino aci
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                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-0228-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-07-757-022B-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 11; DB 4; Length 422; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Genner, Thomas G.
APPLICANT: Glark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
ADDRESSEE: Genetics Institute, Inc.
STRET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MASSACANDSETES
CUNNINY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING APPLICATION: 530
PRIOR APPLICATION S30
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-MG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELESPAX: (617)876-1170
TELESPAX: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUARN
REGISTRATION NUMBER: 31,822
REPERSINGE/DOCKET NUMBER: GI 5190
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 SSSSSSSSST 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-757-022B-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-07-757-022B-66
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ВВ

Mismatches
0;
Conservative
11;
Matches

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0; Gaps

0; Indels

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Search completed: February 19, 2004, 19:39:48 Job time : 22 secs

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sequence 94, Appl Sequence 96, Appl Sequence 96, Appl Sequence 30, Appl Sequence 2074, App Sequence 2074, Appl Sequence 22, Appl Sequence 22, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 32421, Appl Sequence 32421, Appl Sequence 380, Appl Sequence 380, Appl Sequence 380, Appl Sequence 381, Appl Sequence 381, Appl Sequence 382, Appl Sequence 382, Appl Sequence 382, Appl Sequence 383, Appl Sequence 384, Appl Sequence 384, Appl Sequence 1943, Appl Sequence 1943, Appl Sequence 1943, Appl Sequence 1943, Appl Sequence 7924, Appl Sequence 7924, Appl Sequence 7924, Appl Sequence 7924, Appl Sequence 7924, Appl Sequence 7924, Appl Sequence 7924, Appl

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GENERAL INCORPATION:

GENERAL INCORPATION:

APPLICANT: Edinger, Shlowit R

APPLICANT: Edinger, Shlowit R

APPLICANT: Edinger, Shlowit R

APPLICANT: Edinger, Shlowit R

APPLICANT: Edinger, Marzel

APPLICANT: Marzel

APPLICANT: Kekuda, Ramesh

APPLICANT: No. US20040014038Alel GPCR-Like Proteins and Nucleic Acids Encodi

TITLE OF INVENTION: No. US20040014038Alel GPCR-Like Proteins and Nucleic Acids Encodi

FILE REFERENCE: 2103-01-29

FRIOR APPLICATION NUMBER: 60/259,552

PRIOR APPLICATION NUMBER: 60/259,552

PRIOR APPLICATION NUMBER: 60/260,544

PRIOR FILING DATE: 2001-01-09

PRIOR PRILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-09

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 34

LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KINCTGIYLVHLAVSDLLFTVALPGRVVCYVLGSSWPFGKGLCRLTAFVLYTDTYGGVYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIKLGPYFTPPTKIKTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIKLGPYFTPPTKIKTKIKDLNVESQTVKIFLRSLFYTALLVFSALGNILALCLTCQKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 360; DB 12; Length 360; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0;
1 US-10-124-557-92

1 US-10-124-557-94

1 US-10-124-557-94

1 US-10-124-557-96

1 US-10-124-557-96

1 US-10-124-557-96

1 US-09-934-455-96

2 US-10-134-780-2074

2 US-10-134-780-2074

2 US-10-124-557-70

2 US-10-124-557-70

2 US-10-124-557-64

4 US-10-124-557-64

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4 US-10-124-557-64

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6 US-10-124-557-68

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1 US-09-831-545-1720

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4 US-10-124-557-68

5 US-10-124-557-68

6 US-10-124-557-68

6 US-10-123-668-380

6 US-10-133-668-380

6 US-10-153-668-380

7 US-10-153-668-380

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US-10-032-585-7924
US-10-264-049-2651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/10041615
Publication No. US20040014038A1
GENERAL INFORMATION:
           444444444884 848448885540888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
           US-10-041-615-34
           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
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Sequence 109, App
                                                                                                                                                                                               February 19, 2004, 19:37:21 ; Search time 40 Seconds (without alignments) 1884.441 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                      MIKLGPYFTPPTKIKTKD......SETPSITQARGSMFLAEHVV 360
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(cgm2_6/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

(cgm2_6/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

(cgm2_6/ptodata/1/pubpaa/USO6_NEW_FUB.pep:*

(cgm2_6/ptodata/1/pubpaa/NEO8_NEW_FUB.pep:*

(cgm2_6/ptodata/1/pubpaa/PCTUB_PUBCOMB.pep:*

(cgm2_6/ptodata/1/pubpaa/NEO8_NEW_FUB.pep:*

(cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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(cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-615-109
US-10-017-161-1620
US-10-022-798-1294
US-09-901-944B-198
US-09-704-864-1273
US-09-764-864-1273
US-09-764-864-812
US-09-764-864-812
US-09-764-864-812
US-10-148-687-4
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US-10-148-687-812
US-09-764-864-836
US-09-764-864-836
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seq length: 200000000
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Match 1
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Maximum DB
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APPLICANT: SUMA, MAKIKO
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ALYIAMA, YUTAKA
APPLICANT: ALYIAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/2,798
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PLING DATE: 2010-06-18
PRIOR PLING PATE: 2010-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.6%; Score 110; DB 12; Length 323;
Best Local Similarity 100.0%; Pred. No. 8e-96;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 199, Application US/09801944B
Publication No. US20040014169A1
GENERAL INFORMATION;
APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S.
TITLE OF INFORMING NO. US20040014169A1el G Protein-Coupled Receptors
FILE REFERENCE: 00100US1
CURRENT APPLICATION NUMBER: US/09/801,944B
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       CURRENT APPLICATION NUMBER: US/10/017,161
                               CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SEQ ID NO 16-20
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1294, Application US/10292798; Publication No. US20030235833A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , SEQ ID NO 1294

: LENGTH: 323

: TYPE: PRT

: ORGANISM: Homo sapiens

US-10-292-798-1294
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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| Publication No. US20040014038A1 | Sequence 109, Application US/10041615 |
| Publication No. US20040014038A1 | Sequence 109, Application No. US2004001403BA1 |
| APPLICANT: Caman, Stacie J |
| APPLICANT: Edinger, Shlomit R |
| APPLICANT: Edinger, Shlomit R |
| APPLICANT: Edinger, Shlomit R |
| APPLICANT: Reidigaru, Muralidhara |
| TITLE OF INVENTION: No. US2004001403BA1e1 GPCR-Like Proteins and Nucleic Acids Encodi |
| PRICE PEREBRUE: 1400-1233-061 |
| CURRENT APPLICANTON NUMBER: 60/259,552 |
| PRIOR FILING DATE: 2001-01-03 |
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| PRIOR FILING
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                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TPIIYPFASTHYRKWILGILKLKGSSSSSSSSSSTPGKASSETPSITQARGSMFLAEHVV 360
                                                                                                               121 MACVSVDHYPAVVCAHWGPRLRTAGRARLVCVAIWTLVLLQTMPLLLMPMTKPLVGKLAC 180
                                                                                                                                                                                                                                                                                                                                                                                                      241 GCLLTLIMLVAVVVCFSPYHLNIKQFMARGMIHLPSCAERRAFLLSLQATVALMNMVGI 300
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Publication No. US20030143668A1
GENERAL INCRWATION:
APPLICANT: SUWA, WAKIXO
APPLICANT: AKIYANA, YUTAKA
APPLICANT: AKIYANA, YUTAKA
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
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Best Local Similarity 100.0
Matches 110; Conservative
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US-10-041-615-109
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US-10-041-615-109
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Hewlick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS.
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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CUUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
FLING DATE: 16-Apr-2002
CLASSIPICATION: CURROWN:
PRIOR APPLICATION: CURROWN:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.2%; Sco... No. -... 100.0%; Pred. No. -... 0; Mismatches
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
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            PRIOR FILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/218,495
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/186,4E
PRIOR APPLICATION NUMBER: 60/186,4E
PRIOR APPLICATION NUMBER: 60/186,4E
PRIOR APPLICATION NUMBER: 60/194,3
PRIOR PILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR PILING DATE: 2000-04-03
PRIOR PILING DATE: 2000-04-03
PRIOR PILING DATE: 2000-04-03
PRIOR PILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PATENTIN NUMBER: 60/218,3
PRIOR PILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PATENTIN NUMBER: 60/218,3
PRIOR PILING DATE: 2000-07-14
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Publication No. US20020137894A1
GENERAL INFORMATION:
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Best Local Similarity
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Parcdi, Luis A.
Hiebsch, Ronald R.
Lind, Peter
Kayres, Paul S.
Ruff, Valerie
Huff, Rita M.
Wood, Linda S.
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PRIOR PILING DATE: 2000-03-08
PRIOR PLING DATE: 2000-03-08
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PRIOR APPLICATION NUMBER: 60/187,581
PRIOR PLING DATE: 2000-03-08
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PRIOR PLING DATE: 2000-03-08
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APPLICANT: Kaytes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Huff, Valerie
APPLICANT: Hoff, Rita M.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20030003451A1e1
FILE REPERENCE: 00325.US1
CURRENT APPLICATION NUMBER: US/09/791,932
CURRENT FILING DATE: 2001-02-23
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Publication No. US20030003451A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 70; Conservative
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PRIOR FILING DATE: 2000-
PRIOR APPLICATION NUMBER:
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US-09-801-944B-198
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5
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US-00-764-812
Sequence 812. Application US/09764864
Sequence 812. Application US/09764864
Setent No. US20020132753A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 812
LENGTH: 112
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100.0%; Pred. No. 0.023;
tive 0; Mismatches 0; Indels
                                                              PRIOR APPLICATION NUMBER: PCT/USO1/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLICATION NUMBER: PCT/USO1/00664

PRIOR PLICATION NUMBER: PCT/USO1/00669

PRIOR PLICATION NUMBER: PCT/USO1/00669

PRIOR PLICATION NUMBER: PCT/USO1/00668

PRIOR APPLICATION NUMBER: PCT/USO1/00668

PRIOR PLICATION NUMBER: PCT/USO1/00668

PRIOR PLICATION NUMBER: PCT/USO1/00668

PRIOR PLICATION NUMBER: PCT/USO1/00663

PRIOR PLICATION NUMBER: PCT/USO1/00663

PRIOR PLICATION NUMBER: PCT/USO1/00661

PRIOR PLICATION NUMBER: PCT/USO1/00661

PRIOR APPLICATION NUMBER: PCT/USO1/00661

PRIOR APPLICATION NUMBER: PCT/USO1/00661

PRIOR PLICATION NUMBER: PCT/USO1/00661

PRIOR APPLICATION NUMBER: PCT/USO1/00661

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR PLICATION NUMBER: US 99/608,408

PRIOR PLICATION NUMBER: US 09/774,203

PRIOR PLICATION NUMBER: US 09/774,203

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Best Local Similarity 100.
Matches 11, Conservative
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HTWAN GENDE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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ITILE OF INVENTION GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION WHERE: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-04
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APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: P723

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 1273

LENGTH: 94
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                                             TELEARANCE INVIEER: GI 5190

TELEOMMUNICATION INFORMATION:
TELEPHONE: (617)876-5851
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-124-557-12
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
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Patent No. US20020132753A1
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11, Conservative
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; ORGANISM: Homo sapiens
US-09-764-864-1273
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Query Match 3.1%; Score 11; DB 12; Length 187; Best Local Similarity 100.0%; Pred. No. 0.039; Matches 11; Conservative 0; Mismatches 0; Indels
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MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRUT APPLICATION DATE: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <uncernity control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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Publication No. US20020137894A1

GENERAL INFORMATION:

APPLICANT: Turner, Katherine

Clark, Stephen C.

Jacobs, Kenneth

Hewick, Rodney M.

Gener, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
          ; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 187
TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-10-148-687-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                                                                                                  3.1%; Score 11; DB 10; Length 112; 100.0%; Pred. No. 0.025; tive 0; Mismatches 0; Indels
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Publication No. US20030185836A1

GENERAL INFORMATION:

APPLICANT: WINCHARTION:

APPLICANT: SLADE, Martin Basil

APPLICANT: WILLIAMS, Keith Leelie

APPLICANT: WILLIAMS, Keith Leelie

APPLICANT: Wacquarie Research Ltd

ITILE OF INVENTION: Cryptosporidium sporozoite antigens

FILE REPERENCE: 047763-5019-US

CURRENT APPLICATION NUMBER: US/10/148,687

CURRENT APPLICATION NUMBER: PCT/AU00/01492

PRIOR FILING DATE: 2000-12-01

PRIOR FILING DATE: 2000-12-01

PRIOR FILING DATE: 10999-112-01

NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/734,626
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-09-738-626-5042
Sequence 5042, Application US/09738626
Septence 5042, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                             Query Match 3.1
Best Local Similarity 100
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-09-764-864-812
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Gaps

325 SSSSSSSSST 335 |||||||||||| 168 SSSSSSSSST 178

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RESULT 14

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Search completed: February 19, 2004, 19:40:41 Job time : 41 secs

33 GSSSSSSSSS 43

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

February 19, 2004, 19:35:36; Search time 20 Seconds (without alignments) 1731.036 Million cell updates/sec

US-10-041-615-34 360 1 MIKLGPYFTPPTKIKTKIKD.....SETPSITQARGSMFLAEHVV 360 Title: Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

Sequence:

283308 seqs, 96168682 residues Searched:

10 Word size :

218 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description	transcription fact	ν.	ck ta	ethylene responsiv	hypothetical serin	neutrophil protein		hypothetical prote		Ä	WSC4 homolog [impo	conserved hypothet	UTR2 protein - yea	ble memb	AF-9 protein - hum	transcription fact	fibrinogen alpha-I	outD protein - Erw	nucleolus-cytoplas	probable transcrip	ption	transcription fact	related to BCS1 pr	carboxymethylcellu	hypothetical prote	_	autoantigen - huma	. ecdysone-induced p	probable membrane
SUMMARIES	ID	A42098	m	S59537	T51989	T40941	A35419	B40722	T47832	G96544	365	T45525	E83465		863257	139411	S22544	A41932	S28014	B42680	I48694	A49672	A55004	~	803818	301	642		A34598	5036
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de	Query Match	3.1		3.1	3.1	٠.	•	•		٠	•	3.1		•	•	3.1		3.1	•			٠.	•	3.1		٠	3.1			
	Score	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
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trfA protein - sli	ecaysone-induced p steroid hormone re	polymorphic membra	polymorphic membra	polymorphic membra	vitellogenin precu	vitellogenin I pre	ht-en protein - le	protein T16B5.1 [i	glycine-rich prote	probable cytochrom	hypothetical prote	dehydrin - upland	embryonic abundant	hypothetical prote
T14004	B34598 S05979	H86557	E72067	C81601	S28974	T29088	813623	C86242	B85356	T12208 '	S69871	T09876	S04042	T23179
C) C	N (N	N	~	~	N	N	~	N	N	N	N	N	N
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 		3.1		3.1	3.1	3.1	2.8	2.8	œ	œ	80	2.8	8.7	8 14

ALIGNMENTS

RESULT 1 A42098						
transcription factor Oct-2B,	factor	Oct-2B,	octamer-binding	-	human	_
the state of the s						

(fragment)

ö Gaps ö Query Match
3.1%; Score 11; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels

103 SSSSSSSST 113 325 SSSSSSSSST 335 ઠે 셤

Glycine-rich protein [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Spacesion: C88356 (S.Species) (C.Spacesion: C88356 (S.Species) (S.Speci

A, Gene: AT4g30460

A;Nap position: 4 C;Superfamily: glycine-rich cell wall structural protein 1

ö Query Match 3.1%; Score 11; DB 2; Length 162; Best Local Similarity 100.0%; Pred. No. 0.005; Matches 11; Conservative 0; Mismatches 0; Indels

ö

Gaps

324 GSSSSSSSS 334

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GSSSSSSSSSS 79

69

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Denocic procein lin-32 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: B40722; A40720
R;Wang, B.B.; Mueller-Immergluck, M.M.; Austin, J.; Robinson, N.T.; Chisholm, A.; Kenyor
C;Accession: B40722
A;Accession: B40722
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A;Accession: A,Accession
A;Attle: Control of cell fates in the central body region of Caenorhabditis elegans by t
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 05-Nov-1999
C;Accession: A35419
R;Bellavite, P; Bazzoni, F.; Cassatella, M.A.; Hunter, K.J.; Bannister, J.V.
Bicchem. Bicphys. Res. Commun. 170, 915-922, 1990
A;Title: Isolation and characterization of a cDNA clone for a novel serine-rich neutroph A;Reference number: A35419; MUID:90343818; PMID:1696479
A; Residues: 1-262 <LUC>
A; Residues: 1-262 <LUC>
A; Cross-references: EMBL:AL035259; PIDN:CAA22863.1; GSPDB:GN00068; SPDB:SPCC1322.10
C; Genetics:
C; Genetics:
A; Genes: SPDB:SPCC1322.10
A; Map position: 3
C; Superfamily: serine-rich protein
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A; Residues: 36-288 <CLA>
A; Cross-references: GB:L19639; NID:g304331; PIDN:AAC37168.1; PID:g304332
C; Genetics:
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A,Modecule type: mRNA
A,Residues: 1-284 «BEL»
A,Cross-references: GB:M55701; NID:g164672; PIDN:AAA63449.1; PID:g164673
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C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
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Best Local Similarity 100.
Matches 11, Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                  RESULT 3
S5957
heat shock transcription factor HSF21 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Dectes: D5-F6-1996 #sequence_revision 01-Mar-1996 #text_change 02-Sep-2000
C;Accession: S59537, S52303
R;Caznecka-Verner, E; Yuan, C.X.; Fox, P.C.; Gurley, W.B.
R;Caznecka-Verner, E; Yuan, C.X.; Fox, P.C.; Gurley, W.B.
Plant Mol. Biol. 29, 37-51, 1995
A;Title: Isolation and characterization of six heat shock transcription factor cDNA clon A;Reference number: S59537; MUID:96017612; PMID:7579166
A;Reference number: S59537; MUID:96017612; PMID:7579166
A;Reference number: S59537; MUID:96017612; PMID:7579166
A;Reference number: S59537
A;Gatus: nucled acid acid sequence not shown
A;Reference number: BEBI:246952
C;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: tomato heat shock transcription factor HSF24; HSF DNA-binding domain homc C;Keywords: DNA binding; heat shock; leucine zipper; nucleus; stress-induced protein; tr
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R/Lucas, M., Galilardin, C.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. A,Reference number: Z21959
A,Reference number: Z21959
A,Reference number: Z21959
A,Scacssion: T40941
A,Reference number: Data Library, Ganuary 1999
A,Scacssion: T40941
A,Reference number: Data Library, A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,Reference number: A,
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Length 243;

Query Match
3.1%; Score 11; DB 2; Length 243
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 11; Conservative 0; Mismatches 0; Indels

A;Gene: ERF-2

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Length 192;

0; Indels

(Match 3.1%; Score 11; DB 2; I Local Similarity 100.0%; Pred. No. 0.0058; Pes 11; Conservative 0; Mismatches 0;

Query Match Best Local S Matches 11

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hypothetical protein BH0055 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Accession (383656
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirst Nucleic Acids Res. 28, 4317-4311, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: G18566
A;Accession: G18566
A;Accession: G18566
A;Accession: G18566
A;Accession: G18566
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A;Accession: G18566
A;Accession: G18566
A;Accession: G18566
C;Genetics: 1-416 <STO>
A;Accession: G18566
A;Experimental source: strain C-125
C;Genetics: C;Genetics: G18580
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C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Dacession: T45525
R;Bao, W.G.; Fukuhara, H.
Submitted to the RMBL Data Library, July 1999
A;Description: The ubiquitin-encoding genes of Kluyveromyces lactis.
A;Reference number: 223000
A;Steus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-446 <BAO>
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100.0%; Pred. No. 0.012;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.012;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
Matches 11, Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
CiAccession: 47832
RiNyAkatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Submitted to the Protein Sequence Database, February 2000
A; Reference number: 224475
A; Reference number: 224475
A; Residual preliminary
A; Molecule type: DNA
A; Residuale type: DNA
A; Residuale 1996: NAA
A; Residuale 1996: MAA
A; Residuale 1990: Clone 1209
A; Experimental source: cultivar Columbia; BAC clone 7209
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A;Molecule type: DNA
A;Realdues: 1-323 <STO>
A;Cross-references: GB:AE005173; NID:gl1094707; PIDN:AAG29643.1; GSPDB:GN00141
C;Genetics:
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100.0%; Pred. No. 0.0088;
iive 0; Mismatches 0; Indels
                                                                   Indels
0.0083;
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hypothetical protein T209.60 - Arabidopsis thaliana
                           Pred. No. 0.
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C;Superfamily: RING finger homology
F;165-215/Domain: RING finger homology <RRN>
                           Best Local Similarity 100.0%; P: Matches 11; Conservative 0;
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Best Local Similarity 100.
Matches 11; Conservative
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A;Map position: 1
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Search completed: February 19, 2004, 19:39:16
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A; Residues: 1-568 <NAK>
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A; Residues: 1-467 < ADIES.
A; Residues: 1-467 < ADIES.
A; Cross-references: EMBL:U18779; NID:g603625; PID:g603639; MIPS:YEL040w
B; Melnick, L.; Sherman, F.
C. Mol. Biol. 233, 372-238, 193
A; Title: The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Sacchar A; Reference number: S38543; MUID:94016558; PMID:8411151
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NyAlternate names: hypothetical protein N0583

NyAlternate names: hypothetical protein N0583

NyAlternate names: hypothetical protein N0583

C;Secession: S63257

#sequence_revision 03-May-1996 #text_change 06-Feb-1998

C;Accession: S63257

#seference number: S63245

A;Reference number: S63245

A;Reference number: S63245

A;Residues: 1-503 <MES>

A;Residues: 1-503 <MES>

A;Residues: 1-503 <MES>

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UTRZ protein - yeast (Saccharomyces cerevisiae)
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UTRZ protein - yeast (Saccharomyces)
USAlesias: Saccharomyces cerevisiae
C; Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 06-Feb-1998
C; Accession: $30839; $30504; $33845
R;Mulligan, U.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A; Reference number: $30812
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A; Residues: 1-467 < MUL>
A; Across-references: GB:U18779; EMBL:L10830; NID:g603625; PID:g603639
B; Pipetrich, F. S.
submitted to the EMBL Data Library, December 1994
A; Pescription: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.
A; Reference number: $50491
A; Accession: $50504
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100.0%; Pred. No. 0.013;
iive 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 121-129,'V',131-290,'R',292-353,'C',355-467 <MEL>
A;Cross-references: EMBL:S66130; NID:g430829; PID:g430830
C;Genetics:
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A;Cross-references: SGD:S0000766; MIPS:YEL040w
A;Map position: 5L
A, Experimental source: strain PAO1 C, Genetics: A, Gene: PA1451
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Best Local Similarity 100.
Matches 11; Conservative
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RiNakamura, T.; Alder, H.; Gu, Y.; Prasad, R.; Canaani, O.; Kamada, N.; Gale, R.P.; Lang
Proc. Natl. Acad. Sci. U.S.A. 90, 4631-4635, 1993
A;Title: Genes on chromosomes 4, 9, and 19 involved in 11q23 abnormalities in acute leuk
A;Reference number: A47440; MUID:93281633; PMID:8506309
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Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Aug-1997
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A;Gene: SGD:WSC2
A;Cross-references: SGD:S0005227; MIPS:YNL283c
A;Map position: 14L
C;Keywords: transmembrane protein
F;330-346/Domain: transmembrane #status predicted <TWM>
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100.0%; Pred. No. 0.015;
tive 0; Mismatches 0
                                                                                                                                                        3.1%; Score 11; DB 2;
100.0%; Pred. No. 0.014;
tive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: GDB:MLLT3, AF-9
A,Crose-references: GDB:138172, OMIM:159558
A,Map position: 9p22-9p22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: translated from GB/EMBL/DDBJ
                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.1
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                               325 SSSSSSSSST 335
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February 19, 2004, 19:34:31; Search time 17 Seconds (without alignments) 995.860 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                          Run on:
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US-10-041-615-34 360 1 MIKLGPYFTPPTKIKIKD.....SETPSITQARGSMFLAEHVV 360 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

10 Word size : Total number of hits satisfying chosen parameters:

112

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ar c	P32623 saccharomyc			homo	homo	candi			-		E						P17672 drosophila			ichthy		Q9hck8 homo sapien		gossy		^,	096615 galleria me	ß	9evb7	421	P27140 arabidopsis
ID	ERF2 ARATH		WSC2_YEAST	PHR2 CANAL		RN12_HUMAN		FIB2_PETMA	NP14_RAT	CT67_MOUSE	GSQD ERWCH	NFL1 MOUSE	NFL1_HUMAN	GUNA PSEFL	MGPC_MYCGE	E75A_DROME	YL78_YEAST	E75B_DROME	E75C_DROME	PM20_CHLPN	_				DH11_GOSHI	HSB7_HUMAN		SER2 GALME		WR13_ARATH	LYTE_BACSU	CAHC_ARATH
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Length	243	3.4.0	503	546	568	624	634	641	704	706	710	741	772	962	1052	1237	1341	1394	1443	1723	1823	1912	2004	98	145	170	215	220	260	304	n	m
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Score	7.	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	נו	11	11	11	10	10	10	10	10	10	0,	10	10
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090267 brachydanio P87179 schizosacch 091025 gallus gall P18417 catharanthu 060554 mesocricetu 095762 rattus norv P78426 homo sapien 003700 rhizopus ni 022812 caenorhabdi P32583 saccharomyc 016254 homo sapien
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ALIGNMENTS

RESULT 1

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Homeobox; 1.

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ProDom; PD000010; Hos
SMART; SM00389; HOX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A homeotic gene cluster patterns the anteroposterior body axis of C.
                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein lin-39.
LIN-39 OR CEH-15 OR C07H6.7.
Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=93327430; PubMed=8101475;
MISLINE=93327430; PubMed=8101475;
Colark S.G., Chisholm A.D., Horvitz H.R.;
"Control of cell fates in the central body region of C. elegans by the homeobox gene lin-39.";
Cell 74:43-55(1993).
                                                                     .
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MEDLINE=9321429; PubMed=8101474;
Wang B.B., Mueller-Tammergluck M.M., Austin J., Robinson N.T.,
Chisholm A.D., Kenyon C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
Macri C., Vaudin M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COURTOLS THE MICHARION OF NEUROBLASTS AND THE SUBSEQUENT MID-BODY REGION-SPECIFIC DEVELOPMENT.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
-!- SIMILARITY:
                                              Length 243;
                                                                    0; Indels
              192 206 POLY-SER.
243 AA; 26797 MW; C9A4C9791249B5D4 CRC64;
                                             3.1%; Score 11; DB 1; I 100.0%; Pred. No. 0.0045; iive 0; Mismatches 0;
                                                                                                                                                                         253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEL; L19248; AAB04137.1; -...
EMEL; AC06605; AAK65445.1; -...
HSP, P40722; B40722.
HSSP, P02833; 15AN.
WormPep; C07H6.7; CE03975.
TRANSPAC; T03369; -...
InterPro; IPR001827; Antennapedia.
InterPro; IPR001827; Antennapedia.
FEAN, PF00046; homeobox.
PFAN, PF00046; homeobox.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
  AP2/ERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L19639; AAC37168.1; -.
                                             Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                         STANDARD;
                                                                                          325 SSSSSSSST 335
                                                                                                                193 SSSSSSSST 203
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  DNA BIND
DOMAIN
SEQUENCE
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L139_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melnick L., Sherman F.;
"The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
UTS-SRE-2003 (Rel. 42, Last annotation update)
UTR2 protein (Unknown transcript 2 protein).
UTR2 OR YEL040W OR SYGP-ORF18.
Saccharomyces cerevisiae (Baker's yeat).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetacee; Saccharomyces.
PRODOM; FULLY, SMORBER, 1.

RAGATE; SMORBER, 1.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS00012; ANTENNAPEDIA; 1.

PROSITE; PS00012; ANTENNAPEDIA; 1.

PROSITE; PS00012; ANTENNAPEDIA; 1.

POLY-SER,

DOMAIN 12 129 POLY-SER,

POLY-SER,

SITE 148 153 ANTE-TYPE HEXAPEPTIDE.

SITE 165 224 HOMEOBOX.

PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.1%; Score 11; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, S65964; AAD13975.1; -.
EMBL, S66130; AAB28444.1; -.
EMBL, U18779; AAB65002.1; ALT_INIT.
BIR, S30839; S30839.
HSSP, P23904; IAJO.
SQD; S0000766; UTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94016558; PubMed=8411151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 SSSSSSSST 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 SSSSSSSST 34
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STRAIN=S288c / AB972;
PubMed=9169868;
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Gaps

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0; Indels

Length 503;

Score 11; DB 1; 1 Pred. No. 0.0085;

3.1%; SCC_ 100.0%; Pre 0, 1

3.1 Best Local Similarity 100. Matches 11; Conservative

Mismatches

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                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A., Glansdorff N.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
cell wall integrity and stress response component 2 precursor.
WSC2 OR YNL283C OR NO583.
Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota, Saccharomycotina, Saccharomyceses, Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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GO; GO:0004888; F:transmembrane receptor activity; IGI.
GO; GO:000047; P:cell wall organization and biogenesis; IGI.
GO; GO:0009408; P:response to heat; IGI.
GO; GO:0007266; P:Rho protein signal transduction; IGI.
InterPro; IRF002889; WSC.
Pfam; PF01822; WSC. 1.
SWART; SM00321; WSC; 1.
                                                                                                                                                                                                                                                                                                3.1%; Score 11; DB 1; Length 347; 100.0%; Pred. No. 0.0062; ive 0; Mismatches 0; Indels
GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
GO; GO:0000144; C:septin ring (sensu Saccharomyces); IDA.
InterPro; ISR000757; Glyco_hydro_l6.
Ffam; PF00722; Glyco_hydro_l6; 1.
DOMAIN 234 322 SER-RICH.
DOMAIN 134 124 A. RIN REF. 1).
CONFLICT 171 171 A -> R (IN REF. 1).
CONFLICT 234 234 S -> C (IN REF. 1).
SEQUENCE 347 AA; 36692 MW; IEBAFB862C4BB328 CRC64;
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1 23 POTENTIAL.
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PIR, S63257, S63257.
SGD; S0005227, WSC2.
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Best Local Similarity 100.
Marches 11; Conservative
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121
394
429
475
483
498
503 AA;
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P53832;
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CARBOHYD
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                       MON. Cell. Biol. 17:5960-5967(1997).

-i- FUNCTION: REQUIRED FOR AFICAL CELL GROWTH AND FLAYS AN ESSENTIAL ROLE IN MORPHOGENESIS. MAY BE INTEGRAL TO THE PATHOGENIC ABILITY OF THE ORGANISM (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTENDALIAL,
PHIESPONSIVE PROTEIN 2.
REMOVED IN MATURE FORM (POTENTIAL).
SER. RICH.
POLY-SER.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- INDUCTION: REPRESSED AT PH VALUES ABOVE 6 AND PROGRESSIVELY INDUCED AT MORE ACIDIC PH VALUES.
-i- SIMILARITY: Belongs to the GAS1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                          MEDLINE=97459694; PubMed=9315654;
Weblischlegel F.A., Fonzi W.A.;
"PERZ of Candida albicans encodes a functional homolog of the
regulated gene PHR1 with an inverted pattern of pH-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11, DB 1; Length 546; Pred. No. 0.0091; 0; Mismatches 0; Indels
                                                                                                                                            IS-JUL-1998 (Rel. 36, Created)
IS-JUL-1998 (Rel. 36, Last sequence update)
IS-DRC-1998 (Rel. 37, Last amotation update)
pH_responsive protein 2 precursor (PH-regulated protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951EE0DB9489CED6 CRC64;
                                                                                                              546 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF011386, AAB80716.1; -. InterPro, IPR004886; GAS1.
Pfam, PF03198; GAS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58979 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1%; 2
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325 SSSSSSSSST 335
                                                                                                              STANDARD;
                                                                                                                                                                                              pH responsive protein 2 p
PHR2.
Candida albicans (Yeast)
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                               183 SSSSSSST 193
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546 AA;
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                                                                                                                                                                                                                                                                              NCBI_TaxID=5476;
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                                                                                                                CANAL
                                                                                                                                                                                                                                                                                                                                                                                                              expression.
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Matches 11
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DOMAIN
CARBOHYD
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PHR2 CA
013318;
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RESULT

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MEDINE=9281631; PubMed=8506309;
MEDINE=9281631; PubMed=8506309;
MARAMURA T., Alder H., Gu Y., Prasad R., Canaani O., Kamada N.,
Gale R.P., Lange B., Crist W.M., Nowell P.C., Croce C.M., Canaani E.;
Gale R.D. Lange B., Crist W.M., Nowell P.C., Croce C.M., Canaani E.;
Ganes on chromosomes 4, 9, and 19 involved in 11q23 abnormalities in
acute leukemia share sequence homology and/or common motifs.";
Proc. Natl. Acad. Sci. U.S.A. 90:4631-4635(1993).
I. SUBCARILIAR LOCATION: Nuclear (By similarity).
I. SUBCARILIAR LOCATION: Nuclear (By similarity).
I. DISBASE: Involved in acute leukemias by a chromosomal
translocation t(9;11)(p22;q23) that involves MLIT3 and MLL/HRX.
The result is a rogue activator protein.
I. SIMILARITY: TO YEAST TRANSCRIPTION INITIATION PACTOR TPIF SMALL
SUBUNIT (TRG3/ANC1).
SUBUNIT (TRG3/ANC1).
WHWH="http://www.infobiogen.fr/services/chromcancer/Genes/AF9.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                          MLIT3 FOR AFS...
Homo sapiens (Human).
Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-PRO.
MIL FUSION POINT (IN ACUTE MYELOID LEUKEMIA PATIENT CO).
MIL FUSION POINT (IN ACUTE MYELOID INTERMIA PATIENT FI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator; Nuclear protein; Chromosomal translocation; Proto-oncogene.
                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                  PRT; 568 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM, 159558; --
Ol GO:0005634; C:nucleus; TAS.
GO; GO:0007048; P:oncogenesis; TAS.
InterPro; IPROG533; YEATS.
PFGM; PF03366; YEATS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 AA; 63367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L13744; AAA58361.1; -. PIR; 139411; 139411. Genew; HGNC:7136; MLLT3. MIM; 129558; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 11; Conservative
                  STANDARD;
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                                                                                                                AF-9 protein.
                  HUMAN
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AF9_HUMAN
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HGNC:13429; RNF12.
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ZN FING
                                                                                                                          SMART;
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                 3.1%; Score 11; DB 1; Length 568; 100.0%; Pred. No. 0.0095; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                           RN12_HUMAN STANDARD; PRT; 624 AA. Q9NWW2; Q9YSB9; 16-OCT--2001 (Rel, 40, Last sequence update)
                                                                                      325 SSSSSSSSST 335
                                                                                                                       181 SSSSSSSST 191
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RN12_HUMAN

RESULT 7

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RA SEQUENCE FROM N.A.

RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nabikawa T., Nagai K., Shagano S., Shiratori A., Sudo H.,

RA Takahabii M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Takahabii M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Takahabii M., Chiba Y., Ishida S., Murakawa K., Ishii S., Kawai Y., Saito K.,

RA Mamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Ninomiya K., Iwayanagi T.,

RA Ninomiya K., Iwayanagi T.,

RA Ninomiya K., Iwayanagi T.,

RA Ninomiya K., Iwayanagi T.,

RA Ninomiya K., Iwayanagi T.,

RA Ninomiya K., Iwayanagi T.,

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                                                                                                                                                                                                                                                                                      MEDINE-20469411; PubMed=11013082;
Ostendorff H.P., Bossenz M., Mincheva A., Copeland N.G., Gilbert D.J., Jethkins N.A., Lichter P., Bach I.;
"Functional characterization of the gene encoding RLIM, the corepressor of LIM homeodomain transcription factors.";
Genomics 69:120-130(2000).
28-FEB-2003 (Rel. 41, Last annotation update)
RING finger protein 12 (LIM domain interacting RING finger protein)
RING finger LIM domain-binding protein) (R-LIM) (NY-REN-43 antigen)
RNF12 OR KLIM.
Homo sapiens (Human).
ENbaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scanlan M.J., Gordan J.D., Williamson B., Stockert E., Bander N.H., Jongeneel C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Antigens recognized by autologous antibody in patients with renal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 300379; -.

Og. GO:0017053; C:transcriptional repressor complex; NAS.

GO; GO:0003714; F:transcription co-repressor activity; NAS.

GO; GO:0016481; P:negative regulation of transcription; NAS.

InterPro: IPRO01841; Znf ring.

Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER.
S -> C (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00518; ZF RING 1; FALSE NEG. PROSITE; PS50089; ZF RING 2; 1.
Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ271670; CAC14228.1; -.
EMBL; AF155109; AAD42875.1; ALT_FRAME.
EMBL; AK001334; BAA91632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Renal cell carcinoma;
MEDLINE=99438124; PubMed=10508479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Int. J. Cancer 83:456-464(1999).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01d L.J.;
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us-10-041-615-34.oli10.rsp

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EMBL; M84565; AAA73183.1; -.
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CONFLICT
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                     REPEAT
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 X 10 AA TANDEM REPEATS OF [EVIQ]-P-[CDT]-D-[YNW]-P-[PQ]-[QI]-[QP]-[QDN].

1 (APPROXIMATE).

2 (APPROXIMATE).

3 (APPROXIMATE).
                                                                                                                                                                                                                                  HWP1 OR ECE2.
Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                          .
                                                                                                                                                                                                                                                                                                             STRAIN=SC3314;
MEDLINE=96198091; PubMed=8626424;
Staab J.F., Ferrer C.A., Sundstrom P.;
"Developmental expression of a tandemly repeated, proline-and glutamine-rich amino acid motif on hyphal surfaces on Candida albicans.";
J. Biol. Chem. 271:6298-6305 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staab J.F., Ferrer C.A., Sundstrom P.R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: HYPHAL SURFACE. ANTIGEN.
--- SUBCELLULAR FORMION: HYPHAL SURFACE.
--- TISSUE SPECIFICITY: FOUND IN HYPHAL BUT NOT YEAST FORMS.
--- PIM: MAY BE O-GLYCOSYLATED.
                                                    3.1%; Score 11; DB 1; Length 624; 100.0%; Pred. No. 0.01; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Sharkey L.L., Saporito-Irwin S.M., Fonzi W.A., submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
134 N -> D (IN REF. 3).
145 Y -> NR (IN REF. 3).
418 Y -> H (IN REF. 3).
68527 MW, DE3ADE09ACACECF8 CRC64;
                                                                                                                                                                    HWP1 CANAL STANDARD; PRT; 634 AA. P46593; 013424; P87019; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-UL-1999 (Rel. 38, Last annotation update) Hyphal will protein 1 (Cell elongation protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U64206; AAC96368.1; -.
EMBL, AF001978; AAB64014.1; -.
EMBL, U29369; AAC49209.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-225 FROM N.A.
                                                  Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                             324 GSSSSSSSSS 334
                                                                                                                   456 GSSSSSSSS 466
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69
81
81
101
111
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131
 134 1
144 1
418 4
624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=5476;
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DOMAIN 46
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CONFLICT
CONFLICT
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SEQUENCE
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-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGREGATION.
-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAWAS), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMEN, WHICH CLEAVES FIBRINOGEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XITIA WHICH CATALYZES THE BESILON-(GAMA-GLUTDANT)LYSINE CROSS-LINKING BETWEEN GAMAA CHAINS (STRONGER) OF DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Fibrinogen alpha-2 chain precursor [Contains: Pibrinopeptide A].
Petromyzon marinus (Sea lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92196058; PubMed-1549566;
Pan Y., Doolattele R.F.;
"cDMA sequence of a second fibrinogen alpha chain in lamprey: an
archetypal version alignable with full-length beta and gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                    3.1%; Score 11; DB 1; Length 634;
100.0%; Pred. No. 0.01;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        3
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                                                                                                                                                                                                                                                                                      D -> DVPCDNPPQPD (IN REF. 2)

S -> P (IN REF. 2).

S -> P (IN REF. 2).

P -> S (IN REF. 2).

P 941347576BA6376 CRC64;
                10.
11.
12 (INCOMPLETE).
13 (INCOMPLETE) .
14 (INCOMPLETE) .
POLY-GIA.
POLY-THR.
POLY-THR.
                                                                                                                                                                                                                                                                     POLY-VAL
                                                                                                                                                                                                                                                                                                                                                                                 65372 MW;
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Best Local Similarity luv...
Best Local Similarity
Local Similarity
Local Similarity
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    132
11542
11622
11622
1172
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1208
1308
1398
1398
1441
4441
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4441
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TISSUE=Liver;
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150 :
704 AA;
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CT67 MOUSE
AC P59114;
DT 28-FEB-2003
DT 15-SEP-2003
DT 15-SEP-2003
DE CZORF67.
CZORF67.
CS MUS MUSCULUS
CC MUMMALIA; FU
CX NCEL TAXID=1
RN [1]
RN [1]
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VARIANT
SEQUENCE
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REPEAT
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Eukaryota, Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang Y., Isaac C., Wang C., Dragon F., Pogacic V., Meier U.T.;
"Conserved composition of mammalian box H/Ach and box C/D small
nucleolar ribonucleoprotein particles and their interaction with the
common factor Noppl40.",
Mol. Biol. Call 11:567-577(2000).
-: FUNCTION: RELAED TO NUCLEOLOGENESIS, MAY PLAY A ROLE IN THE
MAINTENANCE OF THE FUNDAMENTAL STRUCTURE OF THE FIBRILLAR CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleolar phosphoprotein pl30 (Nucleolar 130 kDa protein) (140 kDa nucleolar phosphoprotein) (Noppl40) (Nucleolar and coiled-body Nosphoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92323542; PubMed=1623516;
Meier U.T., Blobel G.;
"Nopp140 shuttles on tracks between nucleolus and cytoplasm.";
                                                                                                                                               FIBRINOPEPTIDE A (BY SIMILARITY)
                                                                                                                                                                                                                                 STATEMENTY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

INTERCHAIN (WITH BETA CHAIN)

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).
                                                                                                                                                              FIBRINOGEN ALPHA-2 CHAIN.
CLEAVAGE (BY THROMBIN; RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11; DB 1; Length 641;
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
INTERCHAIN (WITH BETA CHAIN)
(BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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CA991A8DD698BFB5 CRC64;
                                                                                                                                                                                                    FIBRINOPEPTIDE A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704 AA.
                           Pfam; PF00147; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FB6; 1.
PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
Blood coagulation; Plasma; Signal; Repeat.
23 POTENTIAL.
PEPTIDE 24 31 FIBRINOPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH NOPS AND FIBRILLARIN. MEDLINE=20143579; PubMed=10679015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%; St.
100.0%; Pred
0; M
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 EMBL; M84482; AAA49264.1; -.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 SSSSSSSST 310
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                                                                                                                                                                641
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                     HSSP; P02671;
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P41777:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation has Bruchean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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AND DENSE FIBRILLAR COMPONENT IN THE NUCLEDLUS. IT HAS INTRINSIC GTPASE AND ATPASE ACTIVITIES. MAY PLAY AN IMPORTANT ROLE IN TRANSCRIPTION CYTALYZED BY RANA POLYMERASE I (BY SMILARITY). SUBUNIT: Interacts with Dkc1/Map57, Nop5/Map65 and fibrillarin. SUBCELLULAR LOCATION: SHUTTLES ON CURVILINEAR TRACKS BETWEEN FUCLEDLUS AND CYTOPLASM. THESE TRACKS STEEND FROM THE DENSE FURILLAR COMPONENT OF THE NUCLEOLUS ACROSS THE NUCLEOLUS TO A LIMITED NUMBER OF WICCLEDLUS ACROSS THE NUCLEOLUS TO A LIMITED REPRESIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION ON CK-II AND PKC SITES. NOPP140 IS ONE OF THE MOST PHOSPHORYLATION ON CK-II AND PKC SITES. NOPP140 IS ONE OF THE SIMILARITY: CONTAINS I LISH domain.
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ACIDIC SERINE CLUSTER 1.
ACIDIC SERINE CLUSTER 2.
ACIDIC SERINE CLUSTER 4.
ACIDIC SERINE CLUSTER 6.
ACIDIC SERINE CLUSTER 6.
ACIDIC SERINE CLUSTER 6.
ACIDIC SERINE CLUSTER 7.
ACIDIC SERINE CLUSTER 7.
ACIDIC SERINE CLUSTER 9.
ACIDIC SERINE CLUSTER 9.
ACIDIC SERINE CLUSTER 9.
ACIDIC SERINE CLUSTER 10.
ACIDIC SERINE CLUSTER 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50896; LISH; 1.

Muclear protein; Phosphorylation; Repeat; GTP-binding; ATP-binding.

LUS 42

LISH.

11 X 12 AA APPROXIMATE REPEATS OF AN DOMAIN

84 570
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 0.011;
0; Mismatches 0; Indels
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15-SEP-2003 (Rel. 42, Last annotation update)
Protein C20orf67 homolog.
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InterPro; IPR006594; LisH.
InterPro; IPR003993; treacle.
Pfam, PF05022; SRP40 C; 1.
PRINTS; PR01503; TREACLE.
SMART; SM00667; LisH; 1.
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Best Local Similarity 100.
Matches 11; Conservative
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CHAIN
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                                        Actausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachline E.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer G.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer G.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mang J., Heish F.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Brichards S., Worley K.C., Hale S., Garchia A.M., Gay L.J., Hulyk S.W.,

Andra S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Andra M., Madan A., Young A.C., Schouchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Broneration and initial analysis of more than 15,000 full-length

Broc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93086427; PubMed=1453958; Condemine G., Dorel C., Hugouvieux-Cotte-Patrat N., Robert-Baudouy J.; Condemine G., Dorel C., Hugouvieux-Cotte-Patrat N., Robert Bruch Gries involved in the secretion of pectate lyases in Erwinia chrysanthemi are regulated by kdgR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erwinia chrysanthemi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
General secretion pathway protein D precursor (Pectic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 3.1%; Score 11; DB 1; Length 706; Local Similarity 100.0%; Pred. No. 0.011; Conservative 0; Mismatches 0; Indels
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MGD, MGILLARASS B. F730014105Rik.
INTERPROJECT: WW.RSP5_WWP.
Ffam; PF00397; WW; 1.
SWART; SWOAF5; WW; 1.
PROSITE; PS01159; WW_DOMAIN 1; FALSE_NEG.
PROSITE; PS01159; WW_DOMAIN 1; FALSE_NEG.
DOMAIN 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    710 AA.
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TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
GSCD_ERWCH
ID GSOD_ERWCH STANDARD;
AC Q01565;
DT 01-JUL-1993 (Rel. 26, Creat
DT 01-MOV-1995 (Rel. 26, Last
DT 01-NOV-1995 (Rel. 26, Last
DE General secretion pathway p
BD General secretion pathway p
COUTD.
OS Erwinia chrysanthemi.
OS Erwinia chrysanthemi.
OS Erwinia chrysanthemi.
OS Bacteria; Proteobacteria; G
OC Bacteria; Proteobacteria; G
OC Bhterobacteriaceae; Pectoba
OX NCBI_TAXID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RX MEDLINE=93086427; PubMed=14
RA CONDEMNIE 93086427; PubMed=14
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Thumb W., Auer M., Stingl G., Baumruker T.,
Th. novel splice variant of the transcription factor Nrfl interacts
with the TNFalpha promoter and stimulates transcription.";
Nucleic Acids Res. 26:2291-2297(1998).
-! FUNCTION: THE SHORT ISOFORM INTERACTS WITH THE EXTENDED KAPPA 3
SITE OF THE TNF ALPHA PROMOTER AFTER PC GAMMA RILL STIMULATION AND
PARTICIPATES IN THE INDUCTION OF THIS CYTOKINE. THE LONG ISOFORM
IS EITHER INACTIVE OR REPRESSES THE TRANSCRIPTIONAL ACTIVATION.
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ID NFL1 MOUSE STANDARD; PRT; 741 AA.

AC 061895; 070234;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Nuclear factor erythroid 2 related factor 1 (NF-E2 related factor 1)

DE (NFE2-related factor 1) (Nuclear factor, erythroid derived 2, like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
MOI. Microbiol. 6:3199-3211(1992).

-:- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.

-:- SUBCELLULAR LOCATION: Outer membrane (Probable).

-:- SIMILARITY: BELONGS TO THE EXED/OUTD/PULD/XPSD FAMILY.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Genomics 25:716-719(1995).
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MEDLINE=98248571; PubMed=9580677;
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PIR, S28014; S28014.

INTERPRO; IPRO01775; BEC GSPD.

INTERPRO; IPRO04846; GSPII/IIIprotein.

INTERPRO; IPRO04845; GSPII/IIIprotein.

INTERPRO; IPRO05644; NolW-like.

Pfam; PF00263; GSPII III; 1.

Pfam; PF00263; GSPII III; 1.

PRINTS; PR00811; BCTERIALGSPD.

PRINTS; PR00811; BCTERIALGSPD.

Transport; Outer membrane; Signal.

SIGNAL.
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MEDLINE=95278942; PubMed=7759107;
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76213 MW;
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Best Local Similarity 100.0
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710 AA;
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Q1444; Q1287; Q967K6;
15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
15-UTL-1998 (Rel. 36, Last sequence update)
15-SPP-2003 (Rel. 42, Last annotation update)
16-SPP-2003 (Rel. 42, Last annotation update)
16-SPP-2003 (Rel. 42, Last annotation update)
16-SPP-2003 (Rel. 42, Last annotation update)
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16-SPP-2003 (Rel. 42, Last annotation factor 1)
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-!- SUBUNIT: HETERODIMER (PROBABLE). IT MAY FORM A HETERODIMER WITH
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1%; Score 11; DB 1; Length 741;
100.0%; Pred. No. 0.012;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    000581;
                                           SEVERAL TRANSCRIPTION FACTORS.
-!- SUBCELLUTAR LOCATION: Nuclear (By similarity)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                   Name=Short;
IsoId=Q61985-2; Sequence=VSP_000580, VSP_
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[1] -SEQUENCE FROM N.A. (ISOFORM 1).

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                                                                                                                                                                                         TISSUE—22388257; PubMed=12477932;

KRIAUREET R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D., Atlausher R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butter R.D., Changel E. M., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Statheton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Anda S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Glubbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubbs R.A., Phey J., Helton E., Ketteman M., Madan A., Scheriguez S., Sanchez A.C., Grimwood J., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and mouse cDNA sequences!", Marra M.A.;

Human and mouse cDNA sequences!", Thuman and mouse cDNA sequences!", Froc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94310069; PubMed=8036168; Caavatta D.J., Townes T.M.; Caterina J.J., Donze D., Sun C.W., Ciaavatta D.J., Townes T.M.; Cloning and functional characterization of LCR-F1: a bZ1P transcription factor that activates erythroid-specific, human globin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression.";
Nucleic Acids Res. 22:2383-2391(1994).
-!- FUNCTION: ACTIVATES ERYTHROID-SPECIFIC, GLOBIN GENE EXPRESSION.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- AUTERNATIVE PRODUCTS.
-:- ALTERNATIVE PRODUCTS.
-:- Event=Alternative splicing; Named isoforms=2;
MEDLINE-95095252; PubMed-8001966;
Luna L., Johnson O., Skartlien A.H., Pedeutour F., Turc-Carel C.,
Prydz H., Kolstoe A.-B.;
Prydz H., Kolstoe A.-B.;
"Molecular cloning of a putative novel human bZIP transcription
factor on chromosome 17q22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q14494-2; Sequence=VSP 000579;
-!- SIMILARITY: Belongs to the bZIP family. CNC subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 163260; --
O GO:0003702; F:transcription cofactor activity; TAS.
GO; GO:0003702; F:transcription factor activity; TAS.
GO; GO:000345; P:embryogenesis and morphogenesis; TAS.
GO; GO:0006783; P:heme biosynthesis; TAS.
GO; GO:0006783; P:inflammatcry response; TAS.
GO; GO:0006954; P:inflammatcry response; TAS.
GO; GO:0006954; P:inflammatcry response; TAS.
INTERPRO; TRR04827; TF bZIP.
PROSITE; PS50217; BZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q14494-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U08853; AAA20466.1; -.
PIR; A49672; A49672.
PIR; A55004, A55004.
HSSP; P34707; ISKN.
Genew; HGNC;7781; NFEZL1.
MIM; 163260; -.
                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                Genomics 22:553-562(1994)
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MEDLINE=89127129; PubMed=2851699;
Hall J., Gilbert H.J.;
Gilbert H.J.;
Gilbert H.J.;
Gilbert H.J.;
Gilbert H.J.;
Gilbert H.J.;
Mol. Gen. Genet. 213:112-117(1988).
Mol. Gen. Genet. 213:112-117(1988).
Inkages in cellulose, lichenin and cereal beta-D-glucosidic
Inkages in cellulose, lichenin and cereal beta-D-glucans.
-:-SIMILARITY: BELONGS TO CELLULASE FAMILY E (FAMILY 9 OF GLYCOSYL
HYDROLASES).
-:-SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)
PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; Activator; DNA-binding; Nuclear protein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UUL-1989 (Rel. 11, Created)
01-UUL-1989 (Rel. 11, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endoglucanase A precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Cellulase) (EGA).
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Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                         Length 772;
                                                                                                                                                                                                                                                                                                                   / Match 3.1%; Score 11; DB 1; Length 772 Local Similarity 100.0%; Pred. No. 0.012; nes 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                  Missing (in isoform 2).
/FTId=VSP 000579.
C868807G6046BEF5 CRC64;
                                                                                    ASP/GLU-RICH (ACIDIC)
                                                                                                                    POLY-SER.
BASIC MOTIF.
LEUCINE-ZIPPER.
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; IPR004197; Glyco hydro 91g.
; IPR000601; PKD domain.
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InterPro, IPR002883; CBD_5.
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                                                                                                                                                                                                                                                                    772 AA; 84703 MW;
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fam; PF00553; CBM 2; 1
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GUNA PSEFL
ID GUNA PSEFL
AC P10476;
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DR PROSITE; PS00695; GLYCOSYL_HYDROL_F9_2; 1.

KW Cellulose degradation; Hydrolase; Glycosidase; Signal.

FT SIGNAL 3 362 BV SIMILARITY.

FT ACT_SITE 523 523 BV SIMILARITY.

FT ACT_SITE 523 523 BV SIMILARITY.

FT ACT_SITE 523 523 BV SIMILARITY.

FT ACT_SITE 523 523 BV SIMILARITY.

FT DOMAIN 608 664 SER-RICH.

FT DOMAIN 866 962 CELLUCOSE-BINDING (BY SIMILARITY).

FT DOMAIN 866 961 BY SIMILARITY.

FT DOMAIN 866 962 CELLUCOSE-BINDING (BY SIMILARITY).

FT DOMAIN 866 961 BY SIMILARITY.

SQ SEQUENCE 962 AA; 100290 MW; 9E93FEIBAC21A898 CRC64;

Autches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

ON 324 GSSSSSSSSS 334

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Db 607 GSSSSSSSSS 617

Search completed: February 19, 2004, 19:37:49
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February 19, 2004, 19:35:01 ; Search time 40 Seconds (without alignments) 2322.473 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	встір	Q9v684 drosophila	Q8mn67 dictyosteli	Q9gub3 dictyosteli	Q8niv1 neurospora	Q95u13 drosophila	Q9vwc2 drosophila	Q9vwc0 drosophila	Q9ndb3 cryptospori	Q9ncr6 cryptospori	Q9ncs0 cryptospori	Q9ncr8 cryptospori	Q9ncr9 cryptospori	Q9u2e9 caenorhabdi	Q9ncs2 cryptospori	Osngn3 corynebacte	073451 human papil
SUMMARIES	ID	Q9V684	Q8MIN67	Q9GUB3	QBNIV1	Q95U13	Q9VWC2	Q9VWC0	Q9NDB3	Q9NCR6	OSNCS0	Q9NCR8	Q9NCR9	Q9U2E9	Q9NCS2	OBNON3	073451
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5 QBNOKI	S QBNOJ1	11 Q8BY58	10 QBGYNO	11 Q8C5W6	5 QBNOI2	S QBNOIL	5 QBNOHO	S QBNOH1	S Q8N0G5	5 Q8NOH2	5 QBNOIO	5 Q8N0G9	S Q8NOI3	10 Q9M0B4	5 QBNOG8	S Q8N0H9	'n	'n	5 OBNOJ0	5 Q8N017	5 QBNOK2	5 Q8N019	10	10	ហ	S Q8NOIS	10 Q43454	11 090670	
138	141	145	146	149	153	156	157	158	158	158	158	159	159	162	165	170	170	173	173	175	178	178	178	178	179	181	193	193	
3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	
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ALIGNMENTS

SUL V68	01-MAY-2000 (TrEMBLrel. 13, Creat 01-MAY-2000 (TrEMBLrel. 13, Last	01-OCT-2002 (TrEMBLrel, 22, Last												-				Ballew R.M., Basu A., Baxendale	Beeson K.Y., Benos P.V., Berman	Borkova D., E	Cherry J.M.,	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann	Fosier C.,	Harris N. L.	Hostin	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketc	AIMMEI B.E., NOGITA C.D., AFAIC C., AFAVICE S., AULP D., LAI	#8000000000000000000000000000000000000	1 9V684 9V684; 1-MAY-2000 11-MAY-2000 11-MAY-2000 G13169 processor of the control of the c
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[1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99265952; PubMed=10331990;
GUO K., Anjard C., Harwood A., Kim H.J., Newell P.C., Gross J.D.;
"A myb-related protein required for culmination in Dicryostelium.";
"A myb-related protein required for culmination in Dicryostelium.";
Development 126:522(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 3 MYB-LIKE DOMAINS.
-!- SIMILARITY: ACGIFFANDED AGGISTALLY.
-!- SIMILARITY: ACGIFFANDED AGGISTALLY.
-!- SIMILARITY: ACGIFFANDED AGGISTALLY.
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3.3%; Score 12; DB 5; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 0; Indels
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Pfam, PR00249; myb_DNa_binding; 3.
SMART; SM0017; SANT; SANT;
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00037; MYB_2; 1.
DNA-binding; Nuclear protein.
SROUNCHCE 580 AA; 66019 MW; F02D9FACB79F3C43 CRC64;
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Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last amnotation update)
Hypothetical protein.
Dictyostellum discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
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Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL; AE003823; AAF58547.1; -.
FlyBase; FBgn0033704; CG13169.
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Best Local Similarity 100.
Matches 12; Conservative
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D7 01-M
D7 01-M
D8 Myb
OS BUXE
OX NCBI
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                                                                                                                                                                                                         Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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3.3%; Score 12; DB 3; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Neurospora genome project; submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AL807374; CAD37056.1; -...
InterPro; IPR000087; Collagen. Pfam; PF01391; Collagen. 1.
Hyporhetical protein 1.
EQUENCE 624 AA; S8999 WW; 73FED5782242E4D9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                   Last sequence update)
Last annotation update)
   624 AA
                                                         Created)
PRT;
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CG32529 OR CG11936 OR CG15619.
                         Q8NIV1;
01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical protein.
B13H18.080.
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Query Match
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MEDLINE=20196006; PubMed=10731132;

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RADAMEN M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

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RADADIN R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley B.M.,

RADADIN R.M., Basu D.A., Buller H., Cadieu E., Center A., Chandra I.,

RADAGON K.Y., Buosam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RADAGON R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RADOGSON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RADADIN K.J., Evangelista C.C., Ferraz C., Ferrar S., Fleischmann W.,

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RADALSIN M., Alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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RADALSIN M., Mattei B., McIntosh T.C., McLeod M.P., Morris J., Morreson D.,

RADAD M. M., Mattei B., McIntosh T.C., McLeod M.P., Morris J., Morreson D.,

Manner M. M., Mattei B., McIntosh T.C., McLeod M.P., Morris J., Morreson D.,

RADAD M. M., Mattei B., McIntosh T.C., McLeod M.P., Morris J., Morreson D.,

RADAD M. M., Mattei B., McIntosh T.C., McLeod M.P., Morreson D.,

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RADAD M. M., Mattei B., McIntosh T.C., McLeod M.P., Morreson D.,

RADAD M. M., Mattei B., McIntosh T.C., McC., McLeod M.P., McC., McLeod M.D., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC., McC
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FlyBase; FBgn0052529; CG32529.
FlyBase; FRGN0055; BAH.
SWART; SM00439; BAH; 1.
SWART; SM00439; BAH; 1.
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
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CG32529 OR CG11936 OR CG15619.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12; DB 5; I
Pred. No. 0.0043;
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100.0%; Pred. No. cor.
... 0; Mismatches
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les 12; Conserv
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                                                                                Ephydroidea; Dro
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Matches
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shue B.C., Scheeler F., Shen H., Shue B.C., Scheeler F., Shen H., Spier B.C., Scheeler F., Shen H., Spier B.C., Stadlinga A.C., Stapleton M., Strong R., Smith T., Spier B., Spradlinga A.C., Turner R., Venter B., Wang K., Wan E., Wang S., Yang S., Yang Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yah R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 23 | SEQUENCE FROM N.A. | Amanatides P.G., Wan K.H., Holt R.A., Calniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A., A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalail M., Kruse D., Lip P., Mattei B., Moshrefi A., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., A Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., A Williams S.M., Zaveri J.S., Smith H.O., Vener J.C., Rubin G.M., Scomitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Berman E., Berman B., Carlson J.M., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M.M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No. 0.0054;
ive 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13,
01-0CT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
CG32529 protein.
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Ashburner M., Gelbart W.W., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Q9NCR6;
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RATAIN-BERKELEY;
RAGINE GENEER SE. HOLD R.A., FORBIS C.A., GOCGAVIR J.D.,
RAGINE R.D. Celniker S.E., Hold R.A., Flokins R.A., Galle R.F.
RAGINE G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.
RAGINE G.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortnam J.R., Yandlal M.D., Zhang O., Chen L.X.,
RAGINE R.A. Levis S.E., Helf G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Benos P.V., Berner B.G., Bandari D., Bolankavo S.,
RABEORO K.Y. Benos P.V., Barner B.P., Bardaria D.,
RABEOR R.Y. Benos P.V., Berner B.P., Brottler P.,
RABEOR R.Y. Benos P.V., Berner B.P., Excitier P.,
RABEOR K.Y. Benos P.V., Berner B.P., Excitier P.,
RABEOR R.Y. Benos P.V., Berner B.P., Brottler P.,
RABEOR R.Y. Cawley S., Dallake C., Devenport L.B., Davies P.,
RABEOR R.Y. Gabriellan A.E., Gatz R., Dewer D., Davies P.,
RABEOR R.Y. Gabriellan A.E., Gatz R., Dewer D., Dew I., Dietz S.M.,
ROGOR K., Comp F. Gorrell J.H., Guz. Galbart W. M., Classer K.,
RABEOR R.Y. Gabriellan A.E., Gatz R.S., Gelbart W. M., Classer R.,
RABEOR R.Y. Gabriellan A.E., Gatz R. R., Houck J.,
RABEOR R.Y. LHAVEY D., Helman T.J., Wei M.-H., Ibegwam C.,
RABELIN R., Malvan F., Kalpen G.H., Ke Z., Kalp D., Lai Z.,
Alalai M., Kalush F., Kalpen G.H., Ke Z., Kalp D., Lai Z.,
Aland B.K., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Alazoko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Alazoko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Alazoko P., Lei Y., McThcob T.C., McHoor D. M., Ralush R.,
Raberon R.W., Moya W., Murphy L., Murny D.M., Nelson D.L.,
RABICTOR R., Malshina N.V. Mobarry C., Murny D.M., Nelson D.K.,
RABICTOR R., Malshina N.Y. Mobarry C., Wang A., Santh T.,
RABEOR R., Reinigton K., Saudesen M., Stung R., Sant B.,
Raberon R., Wang Z.-Y., Wassarman D.A., Walley K., Wu D., Yang G., Zhu X., Smith H.O.,
RABEOR R., More R., Rubing G.M., Venter J., Siden C., Siden-Kiamos B.C., Siden-Kiamos B.C., Stapleton M., Pittman G.S., Pa
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Revans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Butsam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Reriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Feiffer B., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                           Drosophila melanogaster (Fruit 1 ly).

Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha; Ephydroidea, Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                     CG32529 OR CG11936 OR CG15619.
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STRAIN=GCHISSEGA; TISSUE=COCYSE; MEDIINE=20316040; PubMed=10858329; Strong W.B., Gut J., Nelson R.G.; Strong W.B., Gut J., Nelson R.G.; Cloning and sequence analysis of a highly polymorphic Cryptosporidium parvum gene encoding a 60-kilodalton glycoprotein and characterization of its 15- and 45-kilodalton zoite surface antigen products."; Infect. Immun. 68:4117-4134 (2000).
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                   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 2529 AA; 270675 MW; C9331726EE7547D4 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 22, Last sequence update)
15 NoT -2000 (TrEMBLrel. 22, Last annotation update)
15 NoT glycoprotein gpl5 (Fragment).
Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporialidae; Cryptosporidium.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2002 (TrEMBLrel. 22, Last annotation update)
Gp15 antigen (Fragment).
Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                  FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.0035;
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100.0%; Pred
0; M
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Flydase; FBGN005259; CG32529.
Interpro; IPR00104; Antifreeze_1.
Interpro; IPR001025; BAH.
PRINTS; PR00308; ANTIFREEZEI.
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Strong W.B., Gut J., Nelson R.G.;
"Cloning and sequence analysis of a highly polymorphic Cryptosporidium parvum gene encoding a 60-kilodalton glycoprotein and characterization of its 15- and 45-kilodalton zoite surface antigen products.";
Infect. Immun. 68:4117-4134 (2000).
EMBL; AF178695; AAF81989.1; -.
NON TER 104 104
SEQÜENCE 104 AA; 9926 MW; 3461036523B53C2F CRC64;
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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100.0%; Pred. No. 0.0065;
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100.0%; Pred. No. 0.0067;
iive 0; Mismatches 0; Indels
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Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Gpl5 anitgen (Fragment)
Cryptosporidium parvum.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=20316040; PubMed=10858229;
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Best Local Similarity 100.
Matches 11; Conservative
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       SEQUENCE FROM N.A.
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Infect. Immun. 68:4117-4134(2000).
EMBL, AF178693; AAF81987.1; -.
                                                                                                                                                      STRAIN=HGMI0;

MEDLINE=20316040; PubMed=10858229;

Strong W.B., Gut J., Nelson R.G.;

"Cloning and sequence analysis of a highly polymorphic Cryptosporidium parvum gene encoding a 60-kilodalton glycoprotein and characterization of its 15- and 45-kilodalton zoite surface antigen products.";

EMBL; AR178697; AAF81991.1; -.

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SEQÜENCE 59 AA; 5742 MW; D9173B91CB482AA3 CRC64;
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Pred. No. 0.0045;
0; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
01-0CT-2002 (TremBlrel. 22, Last annotation update)
GDIS antigen (Fragment).
Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
0731_TaxID=5807;
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
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Cryptosporidiidae; Cryptosporidium.
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MEDLINE=20316040; PubMed=10858229;
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STRAIN=6HMA1-10;
MEDLINE=203160P bubMed=10858229;
MEDLINE=203160F bubMed=10858229;
Strong W.B., Gut J., Nelson R.G.;
"Cloning and sequence analysis of a highly polymorphic Cryptosporidium parvum gene encoding a 60-kilodalton glycoprotein and characterization of its 15- and 45-kilodalton zoite surface antigen products.";
Infect Immun. 68:4117-4134(2000).
EMBL; AF178691; AAF81985.1; -.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                           "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 283:2012-2018(1998). Britenst, ALI10485; CAB60362.1; WormPep; Y46G5A.20; CE24293. SEQUENCE 109 AA; 11493 MW; 124002FF2443810F CRC64;
                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 11; DB 5; Length 109; 100.0%; Pred. No. 0.0068; tive 0; Mismatches 0; Indels
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Gp15 antigen (Fragment).
Cryptosporidium parvum.
Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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01-OCT-2002 (TrEWBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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MEDLINE=99069613; PubMed=9851916;
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. BRMBL; AP005278; BABDS-18786.1; -- Hypochetical procean; Complete proteome. SEQUENCE 134 AA; 13002 MW; DA00A9CCF281E271 CRC64;
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                                                                                                                       3.1%; Score 11; DB 16; Length 134; 100.0%; Pred. No. 0.0081; ive 0; Mismatches 0; Indels
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